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(54) Title: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

(57) Abstract: The invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin and a method for identification of the specific animal from a given biological sample.

UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION TECHNICAL FIELD

The invention relates to the identification of novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin at species and sub-species sources. The invention also provides a method for the identification of fragments on mitochondrial cytochrome b gene in biological material of unknown origin.

BACKGROUND ART

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A large number of studies in evolutionary biology utilize phylogenetic information obtained from mitochondrial cytochrome b gene. It has been identified a potent molecule to distinguish the phylogenetic depth of different lineages to family, genus and species in molecular taxonomy¹⁻⁶⁶. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in public databases such as GenBank, NCBI (http://www.ncbi.nlm.nih.gov) etc. We have utilized this capacity of cytochrome b gene in establishing the identity of the origin of animal parts and product to its family, genus and species sources. The technique developed is based on a pair of universal primer that can amplify a small fragment of cytochrome b gene from a vast range of animal species. Establishing identity of confiscated animal parts and products is a great challenge to law enforcement agencies because none of the methods available till date is too efficient to reveal the identity of animal remains beyond a reasonable doubt. Morphological markers, described for certain species allow the identification of complete specimen of animals⁶⁷. However, a complete specimen is confiscated very rarely by the investigation agencies; therefore, these marker are not practical in wildlife forensics. The biochemical traits such as the bile characteristics⁶⁸ blood heam analysis^{69,70} etc. have also been employed in wildlife forensic for identification of individual species. The difficulty of these markers are that these markers are limited in number and are rarely found in their natural forms in which these were originally described as the characteristic of a particular species.

The molecular approaches such as micro-satellite based identification⁷¹, Restriction fragment length polymorphism analysis of mitochondrial genes or PCR based species specific STS markers require the prior information of the species to establish the identity^{72,73}. These methods also need a significant amount of DNA material to be analysed. We may not have the prior information about the species origin of confiscated animal parts and product in forensics, therefore, these methods are not really useful and

practical in wildlife identification. The technique invented by us is universal, therefore does not require any background information to establish the identity of any unknown confiscated remains at family, genus and species sources. Being a PCR based procedure it can be applied with trace amount of any biological material. Because the amplicon length is small (472 bp); therefore, it can work perfectly with the mutilated remains, which are commonly seized by the crime investigation agencies. It does not require the large amount of genetic material i.e. DNA to be analyzed to establish the identity, hence, can detect a minute amount of adulteration in food products. The procedure described is simple and very fast. Due to the said advantages, the procedure invented by us is most suited for forensic wildlife identification.

OBJECTS OF THE INVENTION

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The main object of the invention is to identify a fragment on mitochondrial cytochrome b gene capable of significantly discriminating among various evolutionary lineages of different animal species.

Another object is to identify a fragment on mitochondrial cytochrome b gene which is flanked by the highly conserved sequences at a vast range of animal species.

Yet another object is to detect a fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.

Still another object is to develop the universal primers to amplify the fragment on mitochondrial cytochrome b gene using polymerase chain reaction.

Another object is to develop a PCR protocol that works universally with DNA template of any unknown origin (i.e. all the animal species).

Yet another object is to provide a universal method for identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.

Still another object is to provide a universal method of animal identification to establish the crime with the criminal beyond a reasonably doubt.

Another object is provide a universal method to establish the identity of biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

Yet another object is to provide a universal method for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation to the wildlife resources could be controlled.

Still another object is to provide a universal technique to have an idea of the geographical location of the commitment of wildlife crime based on the haplotype of poached animal—identified by the universal primer invented.

Another object is to provide a universal technique of animal identification to detect the adulteration of animal meat/products in vegetarian food product for the purpose of food fortification, by the food fortification agencies.

Yet another object is to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.

Another object is to invent and authenticate a universal technique that can be converted to a (a) 'MOLECUALR KIT' and (b) 'DNA CHIPS' based application to meet the requirements of above objectives.

15 SUMMARY OF THE INVENTION

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Accordingly, the invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin

DETAILED DESCRIPTION OF THE INVENTION

Keeping in view the above objectives, the cytochrome b gene sequences (1140 bp) of 221 distantly related animal species (listed in Table 1) representing various families were obtained from public database NCBI (http://www.ncbi.nlm.nih.gov). These sequences were aligned using the software Clustal X(1.8)(NCBI, USA) and a fragment (of 472 bp, alignment shown in Table 2) of gene was identified which had all the features mentioned above under column 1, 2 and 3 of sub-heading 'Objectives of invention'. As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in Antilope cervicapra and Felis catus; however, 399 to 870 in Homo sapiens sapiens species. Except at few positions (marked as star (*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering Antilope cervicapra as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of Antilope cervicapra:

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A pair of universal primer was designed to amplify this fragment in polymerase chain reaction (PCR). These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398 to 869 of Antilope cervicapra, a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India. These primers work universally because its 3' end are highly conserved amongst a vast range of animal species (shown in Table 2). As mentioned above, the DNA fragment (sequence of which is shown above) targeted by these primers is highly polymorphic inter-specifically; however, it is monomorphic among the individual of same species (Tables 6, 7a, 7b, 7c, .d and 8, respectively). These unique features of the targeted region enable these primers to generate the molecular signatures of an individual species; thereby, enabling them to differentiate amongst the animals of different species (see in Figure 1c). The variation within the fragment amplified by these primers increase with increasing distances of evolutionary lineages of two animals (Table 8). These unique features of the fragment amplified by the universal primers 'mcb398' and 'mcb869' invented by the applicants fulfill the objectives of invention.

Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared in-silico with the signatures already available in public databases (viz., GenBank, NCBI database etc) using 'BLAST software⁷³, it indicates identity of the family, genus or species of the analyzed material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers 'mcb398' and 'mcb869'. The complete procedure involved in the analyses (the word, 'analyses' should be understood with the stepwise procedure to establish the identity of the biological remain of any unknown animal origin for the aims mentioned in columns

1-13 under sub-heading 'Objectives of invention') is briefed under 'Examples 5 and 6, respectively, as well as illustrated in Figures 1a, 1b and 1c, respectively.

BRIEF DESCRIPTION OF DRAWING AND TABLES

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Figure 1a. Illustration of the step-wise procedure involved in *analyses*. The unknown biological material i.e. 'adil.flesh' refers to the confiscated skin mentioned in 'Example 6'. The arrow marks indicate the stepwise procedure involved. The brief description of Figure 1a is as follows:

The biological material i.e. the confiscated skin 'adil.flesh' was subjected to DNA isolation using the standard procedures⁷⁴. The DNA obtained was amplified using the primers 'mcb398' and 'mcb869' in PCR, fractionated in 2% (w/v) agarose gel, visualized and photographed under UV light using Gel Documentation System (Syngene, USA). The lane 'M' shown in the photograph represents the molecular weight marker (Marker XIII, Boehringer mannheim). Lane 1 shows the PCR amplicon (472 bp) obtained from 'adil.flesh' using primers 'mcb398' and 'mcb869'. The PCR amplicon obtained were sequenced at both the strand using "ABI Prism 3700 DNA Analyzes, PE-Applied Biosystems). The chromatogram shows the sequences (about 80 bp long, i.e. between 150-230 bp of sequence (328 bp), revealed from the PCR product of 472 bp length) obtained from 'adil.flesh'.

Figure 1b. Illustrates the further steps involved in analyses. The sequence (328 bp) revealed from 'adil.flesh' was subjected to homology search in nr (i.e. non-redundant) database of Netional Centre for Biological Information (NCBI), USA. The sequences producing significant alignments are shown along with its bits score and E values. It indicates the extent of homology amongst the sequence enquired (i.e. the 328 bp sequence from adil.flesh) and the sequences registered in nr database of NCBI. BLAST analysis revealed the highest homology of the sequence revealed from 'adil.flesh' with the sequence of Panthera pardus (gene bank registration number 'AY005809'), indicating the identity of adil.flesh as that of a leopard (Panthera pardus) origin. Figure 1b further illustrates the multiple alignments of the sequences obtained from reference animals (listed in Table 5) along with the sequence obtained from 'adil.flesh'. The sequences of 'adil.flesh' is similar to the sequences of 'gz1L' further confirming the identity of the source of confiscated remain 'adil.flesh' as that of a Panthera pardus origin.

Figure 1c illustrates the NJ-tree (Neighbor Joining tree) constructed using CLUSTAL X (1.8) from the sequences revealed from 'adil flesh' and reference animals listed in Table 5.

The animals belonging to similar species cluster together; however, the animals of different species group in different clusters. The confiscated material under investigation (i.e. 'adil.flesh') clusters with 'gz1L' (i.e. the known normal leopard 'Panthera pardus') indicating the identity of the species of 'adil.flesh' as that of a Panthera pardus source.

- Figure 2 shows the Agarose gel electrophorogram showing the PCR amplicons (472 bp) obtained from the reference animals of family felidae listed in Table 5, using universal primers 'mcb398 and 'mcb869'. Description of different lanes is as follows:
 - Lanes 1-21: The PCR profiles of the animals 1-21, respectively, listed in Table 5.
- Lane 22: The PCR profiles of DNA isolated from confiscated skin of unknown animal origin 'i.e. adil.flesh'
 - Lane 23: Negative control (no DNA)
 - Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)
 - Figure 3. Shows PCR amplicons obtained from animals listed in Table 9. The primers used in PCR are 'AFF' and 'AFR'. The description of different lanes shown is as follows:
- Lane 1-4: The PCR profiles of animals 1-4, respectively, listed in Table 9, showing amplicons of 354 bp.
 - Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)
 - Figure 4. Shows PCR amplicons obtained from animals listed in Table 12. This experiment demonstrates the universal nature of our primers among a vast range of animal species. Description of different lanes shown is as follows:
 - Lanes 1-23: The PCR profiles of the animals 1-23, respectively, listed in Table 12. The PCR product of 472 bp is amplified universally from all the animal species analyzed.
 - Lane 24: Negative control (no DNA)

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- Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)
- 25 **Table** 1. List of 221 animal species used for *In-silico* analysis to design the universal primers 'mcb398' and 'mcb869'. Table also demonstrate the 'P,S scores' of 'mcb398' and 'mcb869' for different templates. The descriptions of various symbols used in this table are as follows:
 - Symbol (#) refers to Number
- Symbol (*) refers to the animal species which is either protected species (listed in Wildlife (Protection) Act, 1972 (Central Act NO 53 of 1972), or an endangered/rare animal species Symbol (⁵P,S/F) refers to Probability of match and Stability of match of primer 'mcb398' with different templates (i.e. the cytochrome b gene from different species origin). A higher P, S score refers to the higher probabilities of significant amplification of specific

template by the primer. It is calculated by Amplify (1.2) software.

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Symbol (${}^{\Psi}P,S/R$) refers to <u>Probability</u> of match and <u>Stability</u> of match of primer 'mcb869' with different templates. A higher P,S score refers to the higher probabilities of significant amplification of specific template by the primer. It is calculated by *Amplify* (1.2) software.

Table 2. Multiple sequence alignment of 472 bp fragment of mitochondrial cytochrome b gene (identified by inventors to fulfill the requirements of column 1, 2 and 3 mention under sub-heading 'Objectives of invention') of 221 animal species listed in Table 1. Alignments also show the binding sites for universal primers 'mcb398' and 'mcb869'. The symbol (*) refers to the nucleotide bases which are conserved amongst 221 animal species listed in Table 1). The alignments have been done using software CLUSTAL X (1.8). The nucleitide positions that are unmarked are variable amongst 221 animal species analyzed. These variable sites together constitute the molecular signature of an individual species, giving rise to molecular basis of species identification by our primers.

Table 3. Results of the blast analysis of the sequence revealed from 'adil.flesh' in 'mito' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with felis catus cytochrome b gene sequence (genbank registration number NC_001700.1, bits score 365, E value, e-101) registered in NCBI database (bits score 365 and E value e-101). It gives an indication that the species of analyzed material belongs to family felidae. It also fulfills the requirements of column 6 mention above under sub-heading 'Objectives of invention'.

Table 4. Results of the blast analysis of the sequence revealed from 'adil.flesh' in 'nr' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with Panthera pardus cytochrome b gene sequence (genbank registration number AY005809, bits score 603, E value, e-170) registered in NCBI database. It gives an indication that the species of analyzed material belongs to Panthera paurdus origin. It also fulfills the requirements of column 6 mention above under sub-heading 'Objectives of invention'.

Table 5. Reference animal belonging to family felidae selected for comparison with 'adil.flesh' to confirm the findings of BLAST analysis results of which are mentioned in Table 3 and 4, respectively. The animals listed in SN. 1-21 represent different species of family felidae. SN. 22 and 23 are primate species taken for out-group comparisons.

Table 6 Multiple sequence alignments of cytochrome b sequences (328 bp) revealed from 'adil.flesh' and reference animals listed in Table 5. The positions that have a common nucleotide in all the animal species under investigation are shown with a star (*) mark;

however, the positions that are variable in any of the animals under investigation are unmarked. The nucleotides at these positions constitute the molecular signature of an individual species, which are unique and highly specific for its species. These signatures are the molecular basis of identification of individual animal species using our primers 'mcb398' and 'mcb869'.

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Table 7 (Tables 7a, 7b, 7c and 7d). The comparison of the molecular signatures of different animal species investigated along with 'adil.flesh', the confiscated skin of unknown animal origin. This table demonstrates the variable positions (i.e. the positions which are not marked with star (*) symbol in Table 6), amongst the 328 bp fragment revealed from the animals listed in Table 5. The dot (.) mark represents the presence of the similar nucleotide as listed in lane 1 i.e. the sequence from "adil flesh' at that position. It demonstrates that the signatures of each species are unique and specific to its species. The molecular signatures of 'adil.flesh' are comparable (except for position 37 which has a transition from 'T' to 'C') to the molecular signature of 'gz1L' i.e. the known leopard 'Panthera pardus' source, indicating the identity of the source of confiscated skin 'adil.flesh' as that of a leopard 'Panthera pardus' source. The nucleotide variations (at the positions 153, 198, 223, 264, among the known leopards, (i.e. gz1L, gz2L, and gz3L, respectively)), give an idea about the geographical habitat of each animals. Various studies referring to molecular evolution of different animal species support this hypothesis⁷⁵; however, it could further be confirmed by taking the reference animals from different geographical areas and analyzing by our primers 'mcb 398' and 'mcb869'. If we could generate the database of different haplotypes (i.e. habitat specific molecular signatures) of the animal species, it would also enable our primers to reveal the geographical location of the commitment of wildlife crime.

Table 8. Percent similarity matrix calculated by pair-vise comparisons of nucleotide sequences aligned (illustrated in Table 6). The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity (99.7% and 98.2%, with the lineages of animals 'gz2L' and 'gz3L', respectively) with the sequences obtained from known normal leopard source, indicating its identity as that of a leopard origin. The similarity matrix has been calculated using the software PHYLIP (3.5).

Table 9. Animals selected for validation of minimum P,S score for efficient amplification of cytochrome b gene of different origin by the primers 'mcb398' and 'mcb869'. P,S score of primers 'AFF' and 'AFR' for these animals are shown.

Table 10. BLAST analysis of primers 'mcb398' in nr database of NCBI. It demonstrates

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that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer Table 11. BLAST analysis of primers 'mcb869' in nr database of NCBI. It demonstrates that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.

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Table 12. Other animal belonging to distantly related animal species, investigated to confirm the universal nature of primers 'mcb398' and 'mcb869'. Gel photograph showing the PCR amplicons from these animals are shown in Figure 4.

The mitochondrial cytochrome b gene has very widely been used in molecular taxonomic studies. It has immense capabilities to reveal different evolutionary lineages of animals in family, genus and species specific manner. It has also been used to classify the population of a particular species according to its demographic distributions⁷⁵. The vast database of cytochrome b sequences of different animal species has accumulated in public databases such as Genbank and NCBI¹⁻⁶⁵. We have explored these unique characteristics of cytochrome b gene to establish the identity of confiscated remains of any unknown animal by inventing a pair of novel primers, 'mcb398' and 'mcb869', that can amplify a small fragment (472 bp) of cytochrome b gene of wide range of animal species in universal manner. These primers work universally because its 3' ends target within a highly conserved region.

The fragment of cytochrome b gene identified had all the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention'. We identified this fragment by aligning the cytochrome b gene sequences (1140 bp) of 221 different animal species listed in Table 1. These sequences are publicly available in NCBI DNA databases. These sequences were aligned using the software CLUSTAL X (1.8). As mentioned before, the 472 bp fragment of cytochrome b gene identified by us to have the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention' includes the nucleotides between 398 to 869 in Antilope cervicapra and Felis catus; however, 399 to 870 in Homo sapiens sapiens species. Except at few positions (marked as star (*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, revealing the identity of the biological material belonging to that of an unknown animal origin by the procedure invented by us. As for identity of this fragment we are

considering Antilope cervicapra as a representative species, and the sequence the above fragment of cytochrome b gene of Antilope cervicapra is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of Antilope cervicapra

"taccatgaggacaaatatetttttgaggagcaacagteateaceaateteettteageaateeeatacateggtacaaacetagtaga atgaatetgaggagggtteteagtagataaageaaceettaeeegatttttegeetteeaetttateeteeeatttateattgeageeett accatagtacacetactgttteteeaegaaacaggateeaacaaceceacaggaateteateagacgcagacaaaatteeate ceetaetacactateaaagatateetaggagetetaetattaattttaaceeteatgettetagteetatteteaeeggacetgettggag acceagacaactatacaccagcaaacecacttaatacacceccacatateaageeegaatgatactteetatttgeatacgcaateet eegateaatteetaacaaaactaggagg

Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species. Each species in table 2 has been represented by a unique code, which is decoded in Table 1. We selected these species to represent the vast range of animal families of distant orders. Of 221 species, about 65 were the protected/endangered or rare species listed in Wildlife (Protection) Act, 1972 (Central Act NO 53 of 1972). These species are marked with symbol (*) in Table 1. The NCBI accession number refers to its registration number in NCBI database and the number in superscript represent the reference cited. Based on the aligned cytochrome b sequences of different 221 animal species the primers designed were as follow:

Primers name Sequence (5'-3')

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'mcb398' "TACCATGAGGACAAATATCATTCTG"

'mcb869' "CCTCCTAGTTTGTTAGGGATTGATCG"

Tables 2, 10 and 11, respectively, demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed in-silico (In total 221 animal species listed in Table 1 and about 500 species listed in Tables 10 and 11, respectively) Also, the 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software 'Amplify (1.2)', 'Primer3' (http://www.genome.wi.mit.edu/cgi-<u>bin/primer/primer3.cgi</u>) as well as manually. We assigned the P,S score (P=Probability of match, S=Stability of match) to the primers for each template using the software Amplify (1.2). The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98,63 (i.e. the situation where the primer has perfect match with template);

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however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species Talpa europaea whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were Eumeces egregious and Equus ainus. Eumeces egregious had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of Equus ainus was calculated as 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed (AFF= 5'tagtagaatgaatctgaggagg3' and another primer an pair AFR=5'atgcaaataggaagtatcattc3'.) having more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability and lower P, S scores for its templates (listed in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for Platanista gangetica and Sus scrofa These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species Eumeces egregious) for our primers 'mcb398' and 'mcb869', respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species Sus scrofa (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including Eumeces egregious efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

For further confirmation of universal nature of our primers, we blasted the sequence of our primers against the *mito* and *nr* databases of NCBI using BLAST software. The results of these analyses are shown in Tables 10, and 11, respectively.

Finally, the universal nature of the primers was tested in our laboratory with some more animal species listed in Table 12. These primers amplified all the animal species efficiently, giving rise to the band of expected size (472 bp). The results are shown in Figure 4. This experiments substantiated the results of P,S analysis and other *in-silico* analyses to show that the primers 'mcb398' and 'mcb 869' are universal primers.

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The flow chart of establishing identity of the species of biological material of unknown animal origin using primers 'mcb398' and 'mcb869'

Biological material of unknown animal origin

DNA isolation

PCR amplification of DNA isolated using primers 'mcb398' and 'mcb869'

Sequencing at both the strands in triplicate (using any standard procedure of sequencing such as using ABI

Prism 3700, PE-Applied Bio-systems)

BLAST of revealed sequence in mite database in NCBI (http://www.ncbi.nlm.nih.gov/BLAST)

(it gives idea about the family of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

BLAST of revealed sequence in nr database of NCBI

(http://www.ncbi.nlm.nih.gov/BLAST

(it gives idea about the Genus or more precisely, species of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

Selection of reference animals belonging to the family/Genus/and species revealed by mito and nr BLAST searches

Isolation of DNA from the blood of known reference animals; PCR amplification using primers 'mcb398' and 'mcb869'; sequencing of the PCR products in triplicate using the same primers

Multiple sequence alignments of the revealed sequences of mitochondrial cytochrome b gene of known reference animals and the biological material of unknown animal origin using software such as

Autoassembler (/CLUSTAL X (1.8)

Identification of sequence from the aligned sequences

that is homologous (or significantly similar) to the cytochrome b gene sequence of the DNA obtained from biological material of unknown animal origin.

The species of homologous sequence would be the species of the biological material under investigation

Examples

Example 1

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Example for identification of a fragment of cytochrome b gene fulfilling the requirements of columns 1, 2 and 3 mentioned under sub-heading 'Objectives of invention' of heading 'Brief summary of invention'

The cytochrome b molecule has very vastly been used in molecular taxonomic studies. Being a slow evolving gene. It has a tremendous information in its nucleotide sequences to distinguish the animals to their family, genus and species sources 1-65. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in the nr and mito databases of NCBI. We have explored these qualities of cytochrome b gene to establish the identity of confiscated remains of unknown animal origin to its family, genus and species sources. For this purpose, we have identified a fragment of cytochrome b gene which is highly polymorphic inter-specifically, however, it is monomorphic among the individual of same species, therefore it can group the individual of an unknown species with the known individuals of reference species to which it belongs. In order to amplify this fragment from DNA isolated form any unknown origin, it was necessary that it remain flanked with the highly conserved sequences amongst a vast range of animal families. To identify such a unique fragment within the cytochrome b gene, we aligned the sequences of 221 distantly related animal species (listed in Table 1) representing various families using software CLUSTAL X (1.8). These sequences were obtained from public database NCBI (http://www.ncbi.nlm.nih.gov). The aligned data was examined carefully for the conserved sites amongst all the species included in in-silico analysis. We identified a fragment (472 bp) of cytochrome b gene that was fulfilling all the requirements mentioned above and also under column 1, 2 and 3 of sub-heading 'Objectives of invention'.

As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in Antilope cervicapra and Felis catus; however, 399 to 870 in Homo sapiens sapiens species. Except at few positions marked as star (*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering Antilope cervicapra as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of Antilope cervicapra

"taccatgaggacaaatatctttttgaggagcaacagtcatcaccaatctcctttcagcaatcccatacatcggtacaaacctagtaga atgaatctgaggagggttctcagtagataaagcaacccttacccgatttttcgccttccactttatcctcccatttatcattgcagccctt accatagtacacctactgtttctccacgaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaaattccattccac ccctactacactatcaaagatatcctaggagctctactattaattttaaccctcatgettctagtcctattctacacggacctgcttggag acccagacaactatacaccaggaacccacttaatacacccccacatatcaagccgaatgatacttcctatttgcatacgcaatcct ccgatcaattcctaacacaacaaactaggagg"

Example 2:

Example for development of universal primers to amplify the fragment identified mentioned under 'Example 1'.

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A pair of universal primer was designed which has the following features:

- 1. It targets the fragment identified (mentioned under 'Example 1') to amplify it in polymerase chain reaction (PCR).
- 2. Its 3' and 5' ends that are highly conserved (marked as star (*) in Table 2), amongst a vast range of animal species ensuring the amplification of the fragment mentioned above in a universal manner. The sequencing of the fragment amplified by these primes reveals the molecular signature of the species of analyzed material, which on comparison with the sequences of the known reference animals reveals the identity of the species of unknown biological material under investigation.
- 3. The tm (melting temperature) of both primers was almost similar (about 58 degree centigrade) ensuring the significant annealing of both the primers to its template, therefore significant amplification of targeted region in PCR.
 - 4. The internal stability and P, S, score of the primers were ensured higher while designing it. The possibilities of internal loop formation, dimmer formation etc were also excluded by selecting its sequence uniquely. This ensured that the primer would be a good primer to be used in PCR for amplification of DNA from unknown animal origin.
 - 5. The 3' end of the primers were ensured to have either 'G' or 'C' to increase the probability of strong bonding at its 3'ends, which is necessary for efficient amplification of DNA template in PCR. It also strengthens the universal nature of the primer.
 - 6. The sequences of the primers were ensured to be unique so that it does not give rise to non-specific and spurious products in PCR leading to confusion. It improved the efficiency and quality of the technique invented by us.

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7. These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398 to 869 of Antilope cervicapra, a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India.

8. The sequences of the universal primers invented are as follows:

Primers name

Sequence (5'-3')

10 'mcb398'

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"TACCATGAGGACAAATATCATTCTG"

'mcb869'

"CCTCCTAGTTTGTTAGGGATTGATCG"

Example 3:

Example for development of universal PCR conditions to ensure the amplification of a template of any unknown origin in PCR, hence strengthening the universal nature of the technique invented by us

The PCR conditions developed had the following unique features:

- 1 These were capable of amplifying the DNA template of any animal origin in an universal manner using the universal primers mentioned under 'Example 2'.
- 2. The conditions were selected to ensure the comparable annealing temperature for both the primers i.e. 'mcb398' and 'mcb869'.
- 3. The PCR conditions standardized herewith are universal; therefore, the possibility of PCR failure with a template of unknown origin due to non-standard conditions is excluded. It ensures the universal nature of our technique to be used in wildlife forensics.
- 4. The universal conditions mentioned above are:

Amplification reactions should be carried out in 20 μl reaction volume containing approximately 20 ηg of template DNA, 100μm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl₂, 0.5 unit of Ampli*Taq* Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35th cycles should be held for 10 min.

Example 4:

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Establishing the universal nature of our primer and experimental evidences to demonstrate the universal nature of primers:

The universal nature of the primers 'mcb398' and 'mcb 869' was ensured by the following measures:

(a) Selecting the primers from the aligned cytochrome b gene sequences of 221 animal of distantly related species:

The cytochrome b gene sequences (1140 bp) were aligned using software CLUSTAL X (1.8). The region of cytochrome b gene that was most conserved amongst 221 animal species was selected to design the primers.

(b) Selecting the 3' and 5' ends of the primers at the highly conserved positions of cytochrome b gene:

The 3' and 5' ends of the primers were ensured to anneal to a highly conserved position amongst 221 animal species representing a vast range of animal families. It was done to ensure an efficient amplification of all the species in PCR. These positions are shown with star (*) mark in Table 2.

(c) Ensuring either 'G' or 'C' at the 3' end of the primers:

It was ensured the primers to have either 'G' or 'C' at its 3' ends as these are the nucleotides that ensure the strong bonding at the 3' ends of the primers due to three hydrogen bonds while pairing with each other. The strong bonding at 3' ends nelps the primers to anneal properly with its template resulting in significant amplification in PCR.

(d) Selecting the sequences of the primers to ensure a higher internal stability, higher P, S score, and no primer dimmer and loop formation:

The sequences of the primers were selected to have a high P, S score for a vast range of animal species (Shown in Table 1). The care was taken to exclude the possibilities of loop or primer dimmer formation that could reduce the efficiency of the primers in PCR.

(e) Selecting the sequence of the primers with a comparable melting temperature:

The sequences of the primers were selected to have a comparable melting temperature so that these could work together to amplify a DNA template in PCR at a similar annealing temperature. The melting temperature of both the primers was about 58 degree centigrade and the annealing temperature used in PCR is 51 degree centigrade.

Experimental evidences to demonstrate the universal nature of primers:

(1) Evidence from In-silico analysis:

(a) Selecting the primers within the most conserved region of mitochondrial cytochrome b

As mentioned above, the primers were designed to anneal within a highly conserved region of mitochondrial cytochrome b gene fragment of 472 bp. Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species representing a vast range of animal families. The conserved positions of nucleotide sequences are shown with star (*) mark in Table 2

Table 2 also demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico*. In the aligned sequences, the conserved nucleotides are marked with symbol (*). Also, the 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software viz., 'Amplify (1.2)', 'Primer3' (http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi) as well as manually.

(b) P, S, score analysis:

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We assigned the P.S score (P=Probability of match, S=Stability of match) to the primers for each template using the software Amplify (1.2). The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98.63 (i.e. the situation where the primer has perfect match with template); however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species Talpa europaea whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were Eumeces egregious and Equus ainus. Eumeces egregious had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of Equus ainus was calculated as 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another (AFF= 5'ctagtagaatgaatctgaggagg^T and AFR= 5'tatgcaaataggaagtatcattc³'.) that have more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability

and lower P, S scores for its templates (listed in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa* These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egregious*) for our primers 'mcb398' and 'mcb869', respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egregious* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

© BLAST analysis:

The sequences of primers 'mcb398' and 'mcb869' were blasted against mito and nr databases of NCBI to see its significant alignments with the sequences registered in GenBank. As expected, the most significant alignments of the sequences were found with the cytochrome b gene regions (within the 472 bp fragment mentioned in 'Example 1') of different animal species. This analysis also showed that the 3' as well as 5' ends of the primers were highly conserved amongst a vast range of animal species, confirming the universal nature of the primers (Tables 10 and 11, respectively)

(2) Evidence from bench work/experiments done in laboratory conditions:

The DNA from different animals belonging to distantly related species (mentioned in Table 12) was isolated and subjected to PCR amplification using the primers invented by us i.e. the primers 'mcb398' and 'mcb869' The PCR products amplified were resolved in agarose gel by electrophoresis and visualized under UV light. The PCR products of expected size (472bp) were obtained from all the animals confirming the universal nature of our primers. These results are shown in Figure 4.

Example 5:

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Example to establish the identity of confiscated remains from unknown animal original using the universal primers 'mcb398' and 'mcb869'.

The step-vise procedure to establish the identity of the biological material from an unknown animal source is mentioned below:

Biological material of unknown animal origin

DNA isolation

PCR amplification of DNA isolated using primers 'mcb398' and 'mcb869'

Sequencing at both the strands in triplicate (using any standard procedure of sequencing such as using ABI Prism 3700, PE-Applied Bio-systems)

BLAST of revealed sequence in mito database of NCBI

(http://www.ncbi.nlm.nih.gov/BLAST

(it gives idea about the family of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

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BLAST of revealed sequence in nr database of NCBI

(http://www.ncbi.nlm.nih.gov/BLAST

(it gives idea about the Genus or more precisely, species of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

Selection of reference animals belonging to the family/Genus/and species revealed by mito and nr BLAST searches

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Isolation of DNA from the blood of known reference animals;

PCR amplification using primers 'mcb398' and 'mcb869'; sequencing of the PCR products in triplicate using the same primers

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Multiple sequence alignments of the revealed sequences of mitochondrial cytochrome b gene of known reference animals and the biological material of unknown animal origin using software such as Autoassembler/CLUSTAL X (1.8)



Identification of sequence from the aligned sequences

that is homologous (or significantly similar) to the cytochrome b gene sequence of the

DNA obtained from biological material of

unknown animal origin.



The species of homologous sequence would be the species of the biological material under investigation



Application of the above information for the objectives mentioned in columns 7-13 under sub-heading 'Objective of invention' of heading 'Summary of invention'

Example 6:

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The actual execution of the technique invented

As a first application and to demonstrate the ease and utility of this method, we investigated a case of forensic identification submitted at our laboratory to seek scientific opinion on animal hunting evidence. In this case, we received the half burned remains of an unknown animal, confiscated by the crime investigation agencies. The DNA was isolated from the above material following standard methods⁷⁴ and subjected to PCR amplification using the primers mentioned above (viz., 'mcb398' and 'mcb869'). Amplification reactions were carried out in 20 μl reaction volume containing 20 ηg of template DNA, 100μm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl₂, 0.5 unit of Ampli*Taq* Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed were: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35th cycles was held for 10 min.

The PCR products obtained were sequenced in automated work station (ABI Prism 3700, PE-Biosystems) on both strands in triplicate and the sequence resolved (328 bp, shown in Figure 1a) was blasted against *mito* databases of NCBI using BLAST program⁷³. The most significant alignment (bits Value 365, E value e⁻¹⁰¹) of this sequence was produced with the cytochrome b gene sequence of *Felis catus*, (Table 3) indicating that species of

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analyzed material belongs to family felidae. Further, the above sequence revealed from the confiscated remain was blasted against nr databases of NCBI using BLAST program. The most significant alignment (bits Value 603, E value e⁻¹⁷⁰) of this sequence was produced with the cytochrome b gene sequence of Panthera pardus (Table 4), indicating the identity of the analyzed material as that of a Panthera pardus source. Based on this information, we selected the reference animals listed in Table 5 representing different species and subspecies of felidae. The DNA isolated from reference animals was amplified and sequenced on both strands in triplicate using the primer pair mentioned above. Consensus sequences obtained were aligned using program CLUSTAL X (1.8) (Table 6). Sequence comparisons identified 113 variable sites in total amongst all animals analyzed (Table 7). Pair-vise comparisons of sequences were performed to find out the variation among different animals investigated. All the species investigated were differentiated by a their unique nucleotides sequences. The molecular signatures of different reference animals were compared with the molecular signature of the confiscated skin 'adil.flesh'. Table 7 demonstrate that the maximum similarity of the adil.flesh with 'gzll' i.e. known Leopard (Panthera pardus) species, indicating the identity of the adil flesh, the confiscated skin, as that of a Panthera pardus origin. We also calculated the similarity matrix showing the pairvise similarity amongst the animal species under investigation using PHYLIP software This matrix is shown in Table 8. It demonstrates that the animals belonging to different species had more variation; however, the animals of same species had maximum similarity among their cytochrome b sequences. The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity with the sequences obtained from known Leopard source(99.7%, and 98.2 with 'gz11' and 'gz21', respectively); establishing the identity of the source of confiscated material as that of a Normal leopard (Penthera pardus) species. The step-vise procedure involved in above analysis is illustrated in Figure la, lb and lc, respectively.

Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using *BLAST* software⁷³, it indicates identity of the family, genus or species of the analyzed material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers 'mcb398' and 'mcb869'. Application of the information revealed could be in

fulfilling the requirements of objectives mentioned in columns 7-13 under sub-heading 'Objective of invention' of heading 'Summary of invention'

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The method of the invention can be used to establish the identity of confiscated animal parts and products is one of the key requirements of wildlife identification in forensics. It is needed to establish the crime with the criminal beyond a reasonable doubt to avoid the human violation of wildlife resources. Various morphological biochemical and molecular approaches have been given for this purpose; however, none of the current methods is universally applicable to detect the mutilated animal remains of unknown origin. We have identified a fragment on the mitochondrial cytochrome b gene, which has enormous information to differentiate among various animal species back to the family, genus and species sources. We have also found that this fragment is flanked by the highly conserved sequences amongst a vast range of animal species. We invented a pair of universal primer that can amplify this fragment of DNA isolated from the biological material of an unknown animal origin in polymerase chain reaction (PCR) to reveal its identity at species and sub-species sources. This novel invention has great potential to revolutionize the whole scenario of wildlife forensic identification and crime investigation.

Table 1. The animal species included in the study for in-silico analysis

SN.	Code	Name	NCBI accession #	^{\$} P,S/F	₹P,S/R
1	aep.mel	Aepyceros melampus	AF0362891	97,60	94, 62
2	ore.ore	Oreotragus oreotragus	AF0362881	88, 52	94, 62
3	add.nas	Addax nasomaculatus	AF034722 ²	97, 60	95, 66
4	ory.dam	Oryx damah	AJ2226851	90, 58	95, 66
5	hip.equ	Hippotragus equinus	AF022060 ³	98, 63	85.55
6	alc.bus	Alcelaphus buselaphus	AJ222681 ^t	97,60	98, 68
7	sig.lic	Sigmoceros lichtensteinii	AF0349674	97, 60	98, 68
8	bea.hun	Beatragus hunteri	AF0349684	97,60	94, 62
9	dam.lun	Damaliscus lunatus	.AF0166353	97, 60	77,55
10	con.tau	Connochaetes taurinus	AF0166383	82, 56	93, 62
11	bis.bon	Bison bonasus	Y150055	90, 58	87, 63
12	bos.gru	Bos grunniens*	AF0916316	90, 58	94, 62
13	bos.tra	Bos tragocamelus*	AJ2226791.	90, 58	95, 66
	buba.bub	Bubalus bubalis*	D34637 ⁷	97, 60	93, 64
15	buba.ouo bub.min	Bubalus mindorensis	D82895 ⁸	97, 60	87,62
16		Tragelaphus angasii	AF091633°	97, 60	87, 63
17	tra.ang	Tragelaphus eurycerus	AF0362761	90, 58	97, 64
18	nem.cau	Nemorhaedus caudatus*	U17861°	95, 6l	93, 59
19	pse.nay	Pseudois nayaur	AF034732 ²	89, 55	89, 59
20	amm.ler	Ammotragus lervia	AF034731 ²	94, 58	97, 63
21	cap.fal	Capra falconeri*	D8420210	98, 63	95, 66
	cap.ibe	Capra ibex*	AF0347352	98, 63	89, 58
23	hem.jem	Hemitragus jemlahicus*	AF034733 ²	95, 61	90, 61
	гир.руг	Rupicapra pyrenaica	AF034726 ²	95, 61	89, <i>5</i> 9
25	ניםריבי	Rupicapra rupicapra	AF034725 ²	95, 61	94, 64
26	pan.hod	Pantholops hodgsoni	AF034724 ²	98, 63	95, 66
27	bud.tax.tax	Budorcas taxicolor taxicolor*	U17868°	90, 53	95, 66
28	ovi.amm	Ovis ammon*	AF034727 ²	98, 63	97.64
29	ovi.vig	Ovis vignei •	AF034729 ²	98, 63	97.64
30	cap.cri	Capcornis crispus *	AJ30450211	98, 63	94, 63
. 31	ovi.mos	Ovibos moschatus	U17862°	98, 63	92, 61
32	ore.ame	Oreamnos americanus	AF19063212	98, 63	94, 62 90, 61
33	c ep .dor	Cephalophus dorsalis	AF0916346	97, 58	88, 53
34	cep.max	Cephalophus maxwellii	AF096629 ¹³	97, 60 95, 61	93, 59
35	alc.alc	Alces alces	AJ000026 ¹⁴	97, 60	90, 63
36	hyd.ine	Hydropotes inermis	AJ000028 ¹⁴ AF042718 ¹⁵	90, 58	93, 64
37	mun.mun	Muntiacus muntjak*	AB02109816	98, 63	82.59
38	cer.ele.kan	Cervus elaphus kansuensis*	AB021093	98, 63	82. 59
39	cer.ele.xan	Cervus elaphus xanthopygus*	AB021097	98, 63	90.61
40	cer.ele.can	Cervus elaphus canadensis* Cervus nippon centralis	AB02109415	93, 63	90.61
41	cer.nip.ce cer.nip.ye	Cervus nippon vesoensis	AB02109517	98, 63	90.61
43	cer.nip.ye	Cervus nippon keramae	AB021091"	93.63	90, 61
73		CCI vas impjioni ita amas			

			- 14	00 67	00.61
44	cer.nip.pu	Cervus nippon pulchellus	AB02109016	98, 63	90, 61
45	cer.nip.ni	Cervus nippon nippon	AB02109316	98, 63	90, 61
46	cer.ela.sc	Cervus elaphus scoticus	AB02109916	98, 63	90, 61
47	cer.dam	Cervus dama	AJ00002214	98, 63	88, 53
43	ran.tar	Rangifer tarandus	AJ00002914	98, 63	89, 57
49	mos.fus	Moschus fuscus *	AF026333 ¹⁷	90, 59	90, 61
50	mos.leu	Moschus leucogaster*	AF02688917	90, 59	90, 61
51	mos.chr	Moschus chrysogaster *	AF026887 ¹⁷	90, 59	90, 61
52	mos.ber	Moschus berezovskii *	AF026886 ¹⁷	90, 59	90, 61
53	mos.mos	Moschus moschiferus *	AF02688317	90, 59	92, 61
54	kob.ell	Kobus ellipsiprymnus	AF0220593	91,61	95, 66
55	kob.meg	Kobus megaceros	AJ2226861	91,61	83, 56
56	red.aru	Redunca arundinum	AF096628 ¹³	91,61	94, 62
57	red.ful	Redunca fulvorufula	AF036284 ^t	89, 57	94, 62
58	neo.mos	Neotragus moschatus	AJ2226831	89, 57	94, 62
59	pel.cap	Pelea capreolus	AF0220553	91,61	90, 61
60	anticer	Antilope cervicapra*	AF022058 ³	82, 56	93, 64
61	sai.tat	Saiga tatarica	AF06448718	91,61	92, 61
62	gaz.dam	Gazella dama	AF0259543	91,61	92, 61
63	our.our	Ourebia ourebi	AF0362881	82, 56	82, 59
64	gaz.gaz	Gazela gazella *	AJ2226821	91,61	89, 57
65	rap.mel	Raphicerus melanotis	AF0220533	81,54	80, 50
66	mad.kir	Madoqua kirkii	AF022070 ³	90, 58	97,65
67	antame	Antilocapra americana	AF091629 ⁶	98, 63	98, 68
68	tra.jav	Tragulus javanicus*	D3218919	86, 57	86, 59
69	tra_nap	Tragulus napu*	X56288 ²⁰	81, 52	93, 58
70	bal.acu	Balaenoptera acutorostrata	X75753 ²¹	89, 56	97, 61
71	bal.bon	Balaenoptera bonaerensis	X75581 ²¹	89, 56	93, 59
72	bal.bor	Balaenoptera borealis*	X75582 ²¹	89, 56	93, 59
73	bal.edi	Balaenoptera edeni	X75583 ²¹	89, 56	83, 54
74	esc.rob	Eschrichtius robustus *	X75585 ²¹	97, 61	86, 57 93, 59
75	bal.mus	Balaenoptera musculus •	NC_001601 ²²	97, 57	94, 63
76	meg.nov	Megaptera novaeangliae •	X75584 ²¹	97, 61 97, 57	94, 63
77	bal.phy	Balaenoptera physalus *	NC_00132123	93, 55	91,53
78	cap.mar	Caperea marginata	X75586 ²¹	85, 51	33, 55
79	cep.com	Cephalorhynchus commersonii	AF084073 ²⁴ AF084072 ²⁴	85, 51	92, 59
80	cep.eut	Cephalorhynchus eutropia*	AF084072 AF084067 ²⁴	94, 59	92, 59
81	lag.obl	Lagenorhynchus obliquidens Cephalorhynchus heavisidii	AF084070 ²⁴	89, 56	97, 63
82 83	cep.hea	cephalorhynchus hectori	AF084071 ²⁴	89, 56	92, 59
	cep.hec lag.aus	Lagenorhynchus australis	AF084069 ²⁴	86. 54	92. 59
	lag.cru	Lagenorhynchus cruciger	AF08406824	86.54	92.59
	lag.obs	Lagenorhynchus obscurus	AF08406614	86.54	92, 59
	lis.bor	Lissodelphis borealis	AF08406434	85.51	92. 59
	lis.per	Lissodelphis peronii	AF084065*4	86. 54	92, 59
	glo.mac	Globicephala macrorhynchus	AF084055**	94, 59	88, 55
	glo.mel	Globicephala melas	AF084056 ²⁴	94, 59	58.55
	fer.att	Feresa attenuata*	AF084052**	94, 59	92, 59

		AF08405324	94, 59	88,55
92 pep.ele	Peponocephala electra*	AF084059 ²⁴	97,61	89, 59
93 gra.gri	Grampus griscus	AF084057 ²⁴	94, 59	92, 59
94 pse.cra	Pseudorea erassidens*	AF084075 ¹⁴	98, 63	89, 59
95 lag.acu	Lagenorhynchus acutus	AF084061 ²⁴	86, 57	82, 52
96 orci.bre	Orcinus orca		86, 57	91, 54
97 orca.bre	Orcaella brevirostris	AF084063 ²⁴	96, 54	97,63
98 del.cap	Delphinus capensis	AF084087 ²⁴	97, 57	97, 63
99 del.tro	Delphinus tropicalis	AF08408S ²⁴	97, 57	97,63
100 del.del	Delphinus delphis	AF084085 ²⁴	97, 57	97,63
101 stenicly	Stenella clymene	AF084083 ²⁴	97, 57 97, 57	97, 66
102 sten.coe	Stenella coeruleociba	AF084082 ²⁴	97, 57 97, 57	97, 63
103 tur.adu	Tursiops aduncus	AF084092 ²⁴	97, 57 97, 57	97, 63
104 sten.fro	Stenella frontalis	AF084090 ²⁴	-	88, 59
105 saus.chi	Sousa chinensis	AF084080 ²⁴	97, 57	97, 63
106 sten.lon	Stenella longirostris	AF084103 ²⁴	97,61	96, 59
107 turs.tru	Tursiops truncatus	AF08409524	97, 57	97,66
108 lage.alb	Lagenorhynchus alborostris	AF084074 ²⁴	97,61	
109 sten.bre	Steno bredanensis	AF08407724	97, 61	94, 64
110 sota flu	Sotalia fluviatilis	AF304067 ²⁵	97, 61	97, 63 05, 66
111 del.leu	Delphinapterus leucas	U72037 ²⁶	97, 61	95, 66 05, 66
112 mono.mon	Monodon monoceros	U72038 ²⁶	97, 61	95, 66 86, 59
113 plat.gan	Platanista gangetica*	AF304070 ²⁵	97, 61	86, 59
114 plat.min	Platanista minor*	X92543 ²⁷	97, 61	90, 63
115 kogi.bre	Kogia breviceps	U72040 ²⁶	97, 59	92, 63
116 kogi.sim	Kogia simus	AF304072 ²⁸	96, 55 07, 57	80, 58
117 phys.cat	Physeter catodon	AF304073 ²⁵	97, 57	83, 53
118 lipo.vex	Lipotes vexillifer*	AF304071 ²⁵	89, 56 87, 49	92, 62
119 phoc.sin	phocoena sinus	AF084051 ²⁴	96, 55	90, 59
120 berabai	Berardius bairdii	X92541 ²⁷	97, 61	89,57
121 ziph.car	Ziphius cavirostris	X92540 ²⁷	97, 57	90,61
122 meso.eur	Mesoplodon europaeus	X92537 ²⁷	97, 61	92,61
123 meso.bid	Mesoplodon bidens	X92538 ²⁷	91,61	94, 63
124 meso.den	Mesoplodon densirostris	X92536 ²⁷ X92539 ²⁷	97,61	90,65
125 hype.amp	Hyperoodon ampullatus*	AF304074 ²⁵	97, 61	86, 58
126 meso.per	Mesoplodon peruvianus	AF304074	92, 59	88, 55
127 pont.bla	Pontoporia blainvillei	AF304069 ²⁵ Y08813 ²⁹	92, 58	95.66
128 hipp.amp	Hippopotamus amphibius	Y0881429	98, 63	. 97, 66
129 hex.lib	Hexaprotodon liberiensis	AJ245725 ¹⁰	90, 59	87,61
130 rhin.son	Rhinoceros sondaicus*	NC_00180212	90, 59	90, 63
131 cera	Ceratotherium simum	AJ24572310	90, 59	86.57
132 dic.sum	Dicerorhinus sumatrensis	NC_0017853	91,61	73.51
133 equu	Equus asinus Babyrousa babyrussa	Z5010611	39, 56	85.56
134 baby.bab	Phacochocrus africanus	Z5009011	90, 59	87, 54
135 phac.afr 136 sus.scr.ew	Sus scrofa haplosype EWB3*	AF13654914	97. 57	83.54
137 sus.bar	Sus barbatus	Z5010711	97. 57	85.55
138 lama.gla	Lama gluma	U064293	89, 55	85.53
139 lama.gua	lama guanicae	Y088122"	83, 54	86. 57
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					89, 55	85, 53
140	vic.vic	Vicugna vicugna		U06430 ³⁵	94, 58	86, 58
141	cam.bac	Camelus bactrianus		U0642735	97, 60	87, 64
142	arc.for	Arctocephalus forsteri		XS2293 ³⁶	94, 58	87, 64
143	arc.gaz	Arctocephalus gazella		X32292 ³⁶	97, 57	86, 57
	eum.jub	Eumetopias jubatus		X32311 ¹⁶	89, 55	86, 57
	zal.cal	Zalophus californianus		XS2310 ³⁴		81, 52
146	odo.ros	Odobenus rosmarus		X82299 ³⁶	91.61	87, 64
	pho.vit	Phoca vitulina		X32306 ³⁶	90, 58	95, 66
	pho.fascia	Phoca fasciata		X82302 ³⁶	98, 63	
	pho.gro	Phaca groenlandica		X82303 ³⁶	92, 59	90,61
	cys.cri	Cystophora cristata		X82294 ³⁶	89, 56	87, 64
	hyd.lep	Hydrurga leptonyx		X32297 ³⁶	89, 55	82, 54
	lep.wed	Leptonychotes weddelli	•	X72005 ³⁷	98, 63	91,66
	mir.leo	Mirounga leonina		X82298 ³⁶	89, 55	82, 59
	eri.bar	Erignathus barbatus		X3229536	89, 56	87, 63
	mon.sch	Monachus schauinslandi		X72209 ³⁷	91, 61	87, 60
	hela.mal	Helarctos malayanus		U18899 ¹⁸	84, 54	90, 63
	sel.thi	Selenarctos thibetanus		AB02091039	89, 57	87, 64
	ail.ful	Ailurus fulgen *s		X94919 ¹⁰	93, 55	87, 64
159		Felis catus		NC_00170041	85, 56	90, 63
	can	Canis familiaris		NC_00200812	98, 58	84, 54
161		Talpa europaea		NC_00239143	81,50	92, 57
		Glaucomys sabrinus		AF011738	90, 59	82, 54
	gla.sab gla.vol	Glaucomys volans		AB03026145	90, 59	87, 60
	-	Hylopetes phayrei*		AB03025945	91,61	81,50
	hyl.pha	Petinomys setosus*		AB03026045	91,61	81,50
	pet.set	Belomys pearsonii*		AB03026245	91,61	87, 64
	bel.pea	Pteromys momonga*		- AB03026345	97,61	90, 63
	pte.mom gala.demi	Galagoides demidoff		AF27141146	97, 58	87, 64
	pero.pot	Perodicticus potto		AF2714134	97,60	87, 63
	gala.mat	Galago matschiei		AF27140946	97, 60	90, 61
	gala.moh	Galago moholi		AF2714104	97, 57	95, 66
	oto.gar	Otolemur garnettii		AF2714124	92, 58	87, 60
	lor.tar	Loris tardigradus*		U53581 ⁴⁷	97, 60	93, 59
	nyc.cou	Nycticebus coucang*		US3580 ⁴⁷	97.60	95, 66
	mus	Mus musculus		NC_00156948	97, 60	86, 59
	gorr	Gorilla gorilla		NC_0016124	89.57	84, 64 80, 23
	homo	Homo sapiens sapiens		NC_00180750	96, 55	89, 59
178	dug.dug	Dugong dugong*		U07564 ⁵¹	97, 60 97, 60	76.57
	ele.max	Elephas maximus*		AB00241252	97.58	87, 63
130	afr.con	Afropavo congensis		AF013760"	97.57	87.63
181	pavo.mut	Pavo muticus *	1	AF01376353	89.55	35, 57
182	tra.bly	Tragopan blythii*		AF20072254	89.55	86,61
183	tra.sat	Tragopan satyra*		AF229837 ⁵⁴ AF200723 ⁷⁴	39, 55	\$6,61
	tra.cob	Tragopan caboti		AF028802"	89.55	81,56
	tra.tem	Tragopan temmineku*		AF013501"	89, 55	\$7,63
	arg.arg	Argusianus argus		AF028792"	88, 54	85.57
187	cat, wal	Catrous wallichs *				

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188	cro.cro	Crossoptilon crossoptilon*	AF02879453	89,55	85, 57
189	sym.ree	Syrmaticus reevesi*	AF02880153	89.55	85, 57
	bam.tho	Bambusicola thoracica •	AF02879053	80, 48	94, 64
	fra.fra	Francolinus francolinus	AF01376253	97.58	86, 61
	ith.cru	Ithaginis cruentus*	AF06819353	98. 63	85, 57
	ant.par	Anthropoides paradisca	U27557 ⁵⁶	85, 56	82, 58
	ant.vir	Anthropoides virgo	U2754556	84, 54	82, 52
		Grus antigone antigone	U11060 ⁵⁷	90, 53	87, 63
	gru.ant.an	Grus antigone gillae	U11064 ⁵⁷	90, 53	87, 63
	gru.ant.gi	Grus antigone sharpei	U1106157	90, 58	87, 63
	gru.any.sh	Grus leucogeranus*	U27549 ⁵⁶	90, 53	87, 63
	gru.leu	Grus canadensis pratensis	U27553 ⁵⁶	97, 60	87, 63
	gru.can.pr	Grus canadensis rowani	U27552 ⁵⁶	97,60	87, 63
	gru.can.ro	Grus canadensis tabida	U27551 ⁵⁶	98, 63	87, 63
	gru.can.ta	Grus canadensis canadensis	U27554 ⁵⁶	97,61	87, 63
	gru.can.ca		U2755556	90,53	87, 63
	gru.ame	Grus americana	U27546 ⁵⁶	89, 54	87, 63
	gru.gru	Grus grus	U27548 ⁵⁶	90, 58	87, 63
	gru.mon	Grus monacha*	U27547 ⁵⁶	90, 58	87, 63
	gru.nig	Grus nigricollis*	U27550 ⁵⁶	81,54	87, 63
	gru.jap	Grus japonensis	NC_00219658	94, 58	79, 60
	cic.boy	Ciconia boyciana*	AF09033959	93, 63	79, 60
	rhe.ame	Rhea americana	U89190 ⁶⁰	97,61	86, 59
	antalb	Anthracoceros albirostris*	U83310 ⁶¹	97, 61	86, 60
	fal.fam	Falco femoralis	U83311 ⁶¹	97,61	85, 57
	fal.ver	Falco verpertinus	U83307 ⁶¹	97,61	84, 52
	fal.par	Falco peregrinus*	U83306 ⁶¹	92.59	80, 51
	fal.spa	Falco sparverius	NC_000877 ⁶²	98, 63	94, 62
	aytame	Aythya americana	NC_00087959	97.58	90, 61
	smi.sha	Smithornis sharpei	NC_00088028	97,60	87, 64
	vid.cha	Vidua chalybeata	NC_000880	39, 56	86, 57
	chry.pic	Chrysemys picta	AJ131425 ⁶⁴	90, 59	94, 63
	emy.orb.ku	Emys orbicularis	AB012104 ⁶⁵	90, 58	94, 63
220	che.mud	Chelonia mydas *	AB01660655	86, 55	73, 51
221	eum.egr	Eumeces egregius	ABUIOUUU	,	

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Table 2. Multiple sequence alignment of 472 bp fregment of mitochondrial cytochrome b gene of 221 animal species

PRIMER 'mcb393'	TACCATGAGGACAAATATCATTCTG	
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aep.mel	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACAAATCTCCTCTCAGCAA 60	
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cap.fal	TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTTATTACCAATCTCCTCTCAGCAA 60 TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTTATTACCAATCTCCTCTCAGCGA 60	ļ
rup.pyr	TACCATGAGGACAGATATCATTCTGGGGAGCAACAGTTATTACCAACCTCCTCTCAGCGA 60 TACCATGAGGACAGATATCATTCTGGGGAGCAACAGTTATTACCAACCTCCTCTCAGCA 60	
rup.rup	TACCATGAGGACAGATATCATTCTGAGGGGCAACAGTTATTACCAATCTTCTCTCAGCAA 60 TACCATGAGGACAGATATCATTCTGAGGGGCAACAGTTATTACCAATCTTCTCTCAGCAA 60	
nem.cau	TACCATGAGGACAGATATCATTCIGAGGGGCAACAGTTATTACCAACCTCCTCTCAGCAA 60 TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA 60	
bud.tax.tax	TACCATGAGGACAAATATCATT IGAGGAGCAACAG TATACCAACCTCCTTTCAGCAA 60	
pan.hod	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTAATTACCAACCTCCTTTCAGCAA 60 TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTAATTACCAACCTCCTTTCAGCAA 60	
ovi.amm	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCCTTTCAGCAA 60 TACCATGAGGACAAATATCATTCTGAGGAGGACACACTTATTACCAACCTCCTTTCAGCAA 60	,
ovi.vig	TACCATGAGGACAAAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCCTTTCAGCAA 60 ,TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCACCTCCTCTCAGCAA 60	
cap.cri	TACCATGAGGACAAATATCATTCTGAGGGGCTACAGTCATTACTAACCTCCTCTCAGCAA 60 TACCATGAGGACAAATATCATTCTGAGGGGCTACAGTCATTACTAACCTCCTCTCAGCAA 60	
cvi.mos	TACCATGAGGACAAAAA CATACATCATGAGGAGCTACAGTCATCACTAACCTCCTCTCAGCAA 60 TACCATGAGGACAAATATCATTCTGAGGAGCTACAGTCATCACTAACCTACCT	
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cep.dor	TACCATGAGGACAAATATCATTCTGAGGAGCCACAGTCATTACCAACCTCCTCTCAGCAA 60 TCCCATGAGGGCAAATATCATTCTGAGGAGCCACAGTCATTACCAACCTCCTCTCAGCAA 60	
cep.max	TCCCATGAGGGCAAAIAICAIICIGAGGAGGCCACAGTCATTACCAACCTCCTCTCAGCAA 60 TCCCATGAGGACAAATATCATTCTGAGGAGGCCACAGTCATTACCAACCTCCTCTCAGCAA 60	
nod. zid	TCCCATGAGGACAAAAATATCATTTTGAGGAGCAACAGTCATTACCAACCTCCTATCAGCAA 60 TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATTACCAACCTCCTATCAGCAA 60	
bos.gru	TACCATGAGGACAAATATCATTTTGAGGGGCAACAGTCATTACCAACCTCCTATCAGCAA 60 TACCATGAGGACAAATATCATTTTGAGGGGCAACAGTCATTACCACCTATCATCAGCAA 60	
bos.tra	TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTTATTACCAATGTATTATCAGCAA 60 TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTTATTACCAATGTATTATCAGCAA 60	
bub.min	TACCATGAGGACAAAAAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTTCTCTCAGCAA 60 TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACAGTTCTCTCAGCAA 60	
buba.bub	60 AADBACTTCTCAACATAACACTCATCACCAACACTCTCACAAAAAA	
cra.ang	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACAAACCTCCTATCAGCAA 60 TGCCATGAGGACAAATATCATTCTGAGGAGCACGCTCATCACAAACCTCCTATCAGCAA 60	
tra.eur	TGCCATGAGGACAAAAATATCATTTTGAGGAGCAACAGTCATCACAAAACCTTCTATCAGCAA 60 TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATCACCAACACTTCTTCAGCAA 60	
kob.ell	TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA 60 TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA 60	
kob.meg	TACCATGAGGACAAATATCCTTCTGAGGAGCGACAGTCATCACTAATCTCCTTTCAGCAA 60	
red.aru	TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCACTAATCTTCTCTCAGCAA 60 TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCACTAATCTTCTCTCAGCAA 60	
red.ful	TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCACTAACCTTCTCACCAA 60 TGCCATGGGACAAATATCCTTCTGAGGAGCAACAGTTATCACTAACCATTCTACTACGAA 60	
neo.mos	TOCATOGOGACAAATATCCTTCTGAGGAGCAACAGTGATCACGAATGTACTATCAGCAA 60 TGCGATGGGGACAAATATCCTTCTGAGGAGCAACAGTGATCACCAACGTTGTCTCAGCAA 60 TACGATGAGGACAAATATCCTTCTGAGGAGCAACAGTGATCATCACCAACGTTGTCTGAGCAA 60	
pel.cap	TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCACTAACGTCGTCAGCAA 50 TACCATGAGGACAAATATCTTTGTGAGGGCAACAGTTATCACTAACGTCGTCTCAGCAA 50	
gaz.dam		
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gai.tat	TACCATGACCACATATATT OF TANDACIOACIÓN TACTAACCACACACACACACACACACACACACACACACA	
mai.kir	66 AADGATTATOTTOTTOTATATA TAA KADGATTATTATATAA TAA GADGATTATOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOT	
sap.mel	TACCATOROCTOCTOCATO ACTION TO A CARDADOROTTOTTO ACCUARDADOROTTO ACCUARDADOROTTO ACCUARDADOROTTO ACCUARDADOROTTO ACCUARDA	
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hyd.ine	TACCATGAGACAAATATGAGGACGAGAGAGAGAGAGAGAG	
mun.mun alm.alm	TACCATGAGGACAATATCATTCAGGACAAAAAAAAAAAA	
aldiaka Geoleli kan	TACCATGAGGAGAGATATTATTGUGAGGAGGAGGATATTACGAACGTTGTGAGGAA 59 TACGATGAGGAGAAATATGATTGTGAGGAGGAAGAGTTATTACGAACGTTGTGTGAGGAA 59	
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TACCATGAGGACAAATATCATTCTGAGGAGCAACGGTCATTACCAACCTTCTCTCAGCAA 60 cer.ela.xan TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60 cer.ela.can TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA 60 cer.nip.cent TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA 60 cer.nip.yes TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60 cer.nip.ker TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60 cer.mip.pul TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA 60 cer.nip.nip TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTTCTCTCAGCAA 60 cer.ela.sco; TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA 60 cer.dam TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATCACAAACCTCCTCTCAGCAA 60 ran.tar TACCTTGAGGACAAATATCTTTCTGAGGAGCGACAGTTATTACCAATCTTCTCTCAGCAA 60 mos.fus TACCTTGAGGACAATATCTTTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA 60 mos.leu TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA 60 mos.chr TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA 60 mos.ber TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTCATCACTAACCTTCTCTCAGCAA 60 mos.mos tra.jav TACCCTGAGGACAGATATCTTTCTGAGGAGCCACAGTCATCACCAACCTCTTATCAGCTA 60 TACCCTGAGGGCAAATATCTTTTTGAGGAGCTACAGTCATCACTAACCTTCTTTCAGCAA 60 trag.nap TACCCTGAGGACAAATATCATTTTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA 60 bala.acu TACCCTGAGGACAAATATCATTTTGAGGGGCAACCGTCATCACCAACCTCCTATCAGCAA 60 bala.bon TACCCTGAGGACAATATCATTTTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60 bala.bor TACCCTGAGGACAATATCATTTTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60 bala.edi TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACCAACCTCCTATCAGCAA 60 esch.rob TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA 60 bala.mus TACCCTGAGGACAATATCATTCTGAGGCGCAACCGTCATCACCAACCTTCTATCAGCAA 60 mega.nov TGCCCTGAGGACAAATATCATTCTGAGGCGCAACTGTAATCACTAACCTCCTATCAGCAA 60 bala.phy cap.mar TGCCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA 60 cap.mar ceph.com ceph.eut lage.obl ceph.hea TACCCTGGGGACAGATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60 TACCCTGGGGACAGATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60 TACCCTGAGGACAGATATCATTCTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60 TACCCTGAGGACAAATATCATTTTGAGGCGCAACAGTCATCACCAACCTCCTATCAGCAA 60 TACCCTGAGGACAAATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60 ceph.hec TACCCTGAGGACAGATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60 lage.aus TACCCTGAGGACAGATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60 lage.cru TACCCTGAGGACAGATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60 lage.obs TACCCTGAGGGCAGATATCATTTTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA 60 lisso.bor TACCCTGAGGACAGATATCATTTTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA 60 lisso.per TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA 60 clo.mac TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA 60 glo.mel TACCCTGAGGACAGATATCATTCTGAGGGGGCAACCGTCATCACCAATCTCCTATCAGCAA 60 fere.att TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA 60 pepo.ele TACCCTGAGGACAAATATCATTCTGAGGGGGCAACCGTCATCACCAATCTCCTATCAGCAA 60 gram.gri TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTTCTATCAGCAA 60 pse.cra TACCATGAGGACAAATATCATTCTGAGGGGGAACCGTTATCACCAATCTCCTATCAGCAA 60 lage.acu TACCCTGAGGACAGATATCTTTCTGAGGCGCAACCGTCATTACTAATCTCCTATCAGCAA 60 orci.bre TACCCTGAGGACAGATATCCTTCTGAGGTGCAACCGTCATCACCAATCTCCTATCAGCAA 60 crca.bre TGCCCTGGGGACAAATATCATTCTGAGGGGGCAACCGTCATCACCAACCTCTTATCAGCAA 60 del.cap TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60 del.tro TGCCCTGAGGACAAATATCATTCTGAGGGGCAACCGTCATCACCAACCTCTTATCAGCAA 60 del.del TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA 60 sten.cly TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60 sten.coe TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60 tur.adu TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60 sten.fro TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACCAACCTCCTATCAGCAA 60 saus.chi sten.lon TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA 60 TGCCCTGAGGACAAATATCATTCTGAGGGGGAACCGTCATCACCAACCTCTTATCAGCAA 60 turs.tru lage.alb TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACTAATCTCCTATCAGCAA 60 TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATTACCAACCTCCTGTCAGCAA 60 stem.bre TACCCTGAGGACAAATATCATTCTGAGGGGCAACCGTCATTACCAATCTCCTATCAGCAA 60 sota.flu

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del.leu	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATTACCAATCTCCTATCAGCAA	. 63
mono.mon	TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA	. 60
plat.gan	TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTTTTATCAGCAA	. 60
plat.min	TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTTTTATCAGCAA	60
kogi.bre	TACCCTGAGGCCAAATATCATTCTGAGGAGCAACCGTCATCACCAACCTTATATCCGCAA	63
kogi.sim	TGCCCTGAGGCCAAATATCATTCTGAGAGCAACCGTCATCAAAACCTTATATCCCCAA	5.0
phys.cat	AADDADTATOTTODAGAAADAADTOTTADDAGDODAGTTATCAGAAGAGAGAGTATOTA	6.0
lipo.vex	TACCCTGAGGACAAATATCATTTTGAGGCGCAACCGTCATCACTAATCTTCTATCAGCAA	60
phoc.sin	AGOCCTGGGGACAATATCATTTGAGGTGCTACCGTCATCAAACCTCTTATCACCAAACGGGGGGACAAACCTCTTATCACTTTGAGGGTGCTACCGTCATCAACAAACCTCTTATCACAAACACTCTTATCACGTCATCACAAACCTCTTATCACAAACACTCTTATCACAAAACCTCTTATCACAAAACCTCTTATCACAAAACACTCTTATCACAAAACACTCTTATCACAAAACACTCTTATCACAAAACACTCTTATCACAAAACACTCTTATCACAAAACACACAAAACACACAAAACACACAAAAACACAC	60
bera.bai	TGCCTTGAGGGCAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTCCTATCCGCTA	60
ziph.car	TACCTTGAGGACAAATATCATTCTGAGGTGCAACGGTCATCACAAACGTCTTATCCGCTA	60
meso.eur	TTCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATTACCAACCTCCTATCCGCCA	60
meso.bid	TACCCTGAGGACAAATATCATTCTGAGGCGCAACTGTTATTACTAACCTCCTATCCGCTA	60
meso.den	TACCATGAGGACAAATATCCTTCTGAGGTGCAACTGTCATTACCAATCTTCTATCCGCTA	60
hype.amp	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCCGCCA	60
meso.per	TACCTTGAGGACAAATATCATTCTGAGGCGCAACTGTCATTACTAATCTTTTATCTGCTA	60
pont.bla	TACCCTGAGGACAAATGTCATTCTGAGGTGCCACTGTCATCACCTAACCTCCTATCAGCGA	60
hex.lib	TACCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACCAACTTACTATCAGCTA	63
hipp.amp	TGCCATGAGGACAAATGTCATTCTGAGGGGCAACAGTCATTACCAACTTACTGTCAGCTA	60
dic.sum	TACCATGAGGTCAAATATCCTTCTGAGGAGCCACAGTTATCACAAATCTCCTCTCAGCCA	60
rhin.son	TACCATGAGGTCAAATATCCTTCTGAGGGGGCTACAGTCATTACAAATCTCCTCTCAGCCA	60
cera	TACCATGAGGCCAAATATCCTTCTGAGGGGCTACAGTCATCACAAACCTCCTCTCAGCTA	60
edra	TACCATGAGGACAAATATCCTTCTGAGGAGCAACGGTCATTACAAACCTCCTATCAGCAA	୍ଟେ
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pho.vit	TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATCACCAATCTACTATCAGCAA	60
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bala.edi	CAACACTAACACGCTTTTTTGCCTTCCACTTTATCCTCCCCTTCATTATTCTAGCACTAG CAACACTAACACGCTTTTTTTGCCTTCCACTTTATCCTCCCTTCATTATTCTAGCACTAG	133
esch.rob	CAACACTAACACGCTTCTTTGCCTTCCACTTCATCCTTCCATTCATT	130
bala.mus	CAACACTAACACGCTTCTTTGCCTTCCACTTCATTCTCCCCTTCATCATTATAGCATTAG	130
mega.nov	CAACACTAACACGTTTCTTTGCTTTCCACTTCATCCTCCCCTTCATCATTACACCATTAG	130
bala.phy	CAACACTAACACGCTTTTTGCCTTTCACTTTATCCTCCCTTCATCATCATCATCATATCACCATA	130
cap.mar	CGACACTAACTCGCTTCTTTGCTTTCACCTTCATCCTCCCTTTTCATCATTCAT	183
ceph.com	CAACACTAACACGCTTTTTCGCCTTCGACTTTATCGTCCCATTCALCALCACACALTAC	130
ceph.eut	CAACACTAACACGCTTTTTCGGCTTTCACTTTATGCTCCTATTCATCATCACACACA	
lage.obl	CAACACTAACACGCTTTTTCCCTTTTCACTTTATCCTCCATTCATCATCACCAC	133
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Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

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Quary-

(328 letters)

Database: Sequences from complete mitochondrial genomes 129 sequences; 3,164,247 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAOS

Taxonomy reports

Distribution of 80 Blast Hits on the Query Sequence

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ref NC 001700.11 ref NC 001325.11 ref NC 002008.11 ref NC 001602.11 ref NC 000884.11

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Sequences producing significant alignments: (bits) Value

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Felis catus mitochondrion, complete genome	365	e-101
Phoca vitulina mitochondrion, complete genome	198	1e-51
Canis familiaris mitochondrion, complete g	190	4e-49
Halichoerus grypus mitochondrion, complete	180	3e-46
Cavia porcellus complete mitochondrial genome	176	5e-45
Ceracotherium simum mitochondrion, complet	155	2e-41
Myoxus glis mitochondrion, complete genome	153	8e-38
Equus asinus mitochondrion, complete genome	151	3e-37
Orycteropus afer complete mitochondrial ge	149	1e-36
Dasypus novemcinctus mitochondrion, comple	141	3e-34
R.unicornis complete mitochondrial genome	135	2e-32
Mus musculus mitochondrion, complete genome	133	7e-32
Hippoporamus amphibius mirochondrion, comp	125	2e-29
Equus caballus mitochondrion, complete genome	125	2e-29
Macropus robuscus mitochondrion, complete	123	7e-29
Sus scrofa mitochondrion, complete genome	121	3e-28
Rattus norvegicus mitochondrial genome	121	3e-28
Bos taurus mitochondrion, complete genome	121	3e-28
Pan troglodytes mitochondrion, complete ge	117	4e-27
Ovis aries mitochondrion, complete genome	109	1e-24
Talpa europaea mitochondrion, complete genome	103	7e-23
Oryccolagus cuniculus mitochondrion, compl	103	7e-23
Pan paniscus mitochondrion, complete genome	101	3e-22
Human mitochondrion, complete genome	98	4e-21
Balaenoptera musculus mitochondrion, compl	98	4e-21
trainers ismaicensis mitochondrion, comple	<u>95</u>	2e-20
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Mustelus manazo mitochondrion, complete ge	50	9e-10
Gallus gallus mitochondrion, complete genome	58	3e-09
Carassius auratus mitochondrion, complete	56	1e-08
Loxodonta africana mitochondrion, complete Falco peregrinus mitochondrion, complete g	56	1e-08
Rhea americana mitochondrion, complete genome	56	1e-08
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Salmo salar micochondrion, complete genome	54	5e-08
Polypterus ornatipinnis mitochondrion, com	54	Se-08
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Alignments

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NC 000845 16	128ca	. 16144
NC 001911 14		
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NC 001951 14	126	
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Database: Sequences from complete mitochondrial genomes Posted date: Jun 28, 2000 10:56 AM Number of letters in database: 3,164,247 Number of sequences in database: 129

Lambda 1.37 0.711 1.31

Gapped nbda K H 1.37 0.711 Lambda 1.31

Matrix: blastn matrix:1 -3 Gap Penalties: Existence: S, Extension: 2 Number of Hits to DB: 788 Number of Sequences: 129 Number of extensions: 788 Number of successful extensions: 168 Number of sequences better than 10.0: 77 length of query: 328 length of database: 3,164,247

effective HSP length: 15

effective length of query: 313 effective length of database: 3,162,312

effective search space: 989803656 effective search space used: 989803656

T: 0 A: 30 X1: 6 (11.9 bits) X2: 15 (29.7 bits) S1: 12 (24.3 bits)

SZ: 14 (28.2 bits)

BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593400-28182-3122

Query-

(328 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAOS

Taxonomy reports

Distribution of 50 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments	
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Score

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(bica) Value
 Sequences producing significant alignments:
                                                                                                                    603 e-170
 gb[AY005809.1] Panthera pardus cytochrome b gene, partial c...
                                                                                                                    527 e-147
gb|AF053054.1|AF053054 Panthera tigris sumatrae isolate Sul...
gb|AF053053.1|AF053053 Panthera tigris tigris isolate 87 mi...
gb|AF053050.1|AF053050 Panthera tigris corbetti isolate C2 ...
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                                                                                                                    476 e-132
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                                                                                                                    450 e-127
 gb/AF053025.1/AF053025 Panthera tigris tigris isolate 89 Cy...
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gb[AF051021.1 | AF051021 Panthera tigris tigris isolate B5 cy...
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Gb[AF053018.1]AF053018 Panthera tigris tigris isolate 82 cy...
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GD|AF053051 1|AF053051

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GD|AF053047 1|AF053047

GD|AF053046 1|AF053046

GD|AF053045 1|AF053046

GD|AF053044 1|AF053046

GD|AF053042 1|AF053042

GD|AF053041 1|AF053041

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Fanthera tigris sumatrae isolate Sul...

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cb|AF053036.1|AF053036

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pb|AF053035.1|AF053036

panthera tigris altaica isolate S11 ...

panthera tigris altaica isolate S11 ...

panthera tigris altaica isolate S10 ...

panthera tigris altaica isolate S20 ...

panthera tigris altaica isolate S3 c...

panthera tigris altaica isolate S3 c...

panthera tigris altaica isolate S7 c...

panthera tigris altaica isolate S7 c...

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panthera tigris altaica isolate Sc...

panthera tigris altaica isolate Sc...
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AF053035	487	gξ	546
AF053034	487	A	340
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AF053019	547	
AF053043	547	
X82301	54.7	
AF051052	547	
X82300	547	_
AB004238	547	
A3004237	547	
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<u>U20753</u>	417	
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AF125144	417	
AF154975	547	
AB051237	547	t.att.a 476
<u> AF125149</u>	417	
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AF053024	607	
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AF053022	607	
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AF053019	607	
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AF053019	607	g.g.g
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AF053052	607	
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AB004237	607	
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	607	666
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AF125112	477	
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AF053053	667		726
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AF053046	667	t.actga.c	726
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AF053019	667		25
AF053043	667		26
X32301	667		125
AF053052	667	, F. d	26
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AB004238	667		26
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AF154975	667		
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AFOSIO24	727		95
AF053023	727	7	86
AF051022	727		86
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AFOSJOSI	727		'85 '85
AF751049	727		85
AF951047	727	7	85
AF751945	727		85
AF751745	727 727		55
AFDSJ941	727		96
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AF053038	727	786
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AF053037	727	
<u> AF053036</u>	727	786
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AF053034	727	
AF053033	727	a
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AF053029	727	786
AF051028	727	786
AF053027	727	
AF053026	727	d
AF053020	727	cc786
AF053019	727	
AF053043	727	a
X82301	727	a
AF053052	727	atct.cct.c
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X82300		t
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AB004237	727	rt
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AF125149	597	
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AF053050	787	t
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X82300	787	.gc	814
AB004238	787		
AB004237	787		814
	787		614
X82296			15851
NC 001700	15824		15851
U20753	15824	ta	
AF125144	657	c	664
AF154975	787	caa	803
		ca	803
AB051237	787		664
AF125149	657	c	•••

Database: nt

Posted date: Mar 2, 2001 12:20 AM Number of letters in database: 2,861,827,895 Number of sequences in database: 807,597

Lambda K H 1.37 0.711 1.31

Gapped Lambda K H

1.37 0.711 1.31

Matrix: blastn matrix:1 -3 Gap Penalties: Existence: 5, Extension: 2 Number of Hits to DB: 460542 Number of Sequences: 807597 Number of extensions: 460542 Number of successful extensions: 22671 Number of sequences better than 10.0: 6487 length of query: 328 length of database: 2,863,827,885 effective HSP length: 20 effective length of query: 308 effective length of database: 2,847,675,945 effective search space: 877084191060 effective search space used: 877084191060 T: 0 A: 30 X1: 6 (11.9 bits) X2: 15 (29.7 bits) S1: 12 (24.3 bits) S2: 19 (38.2 bits)

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Table 5. Reference animals and the allocated code numbers included in the study

SN	I. Code number	Name of the animal	Zoological name
1	bhz25t	Indian tiger	Panthera tigris tigris
2	bhz26t	Indian tiger	Panthera tigris tigris
3	bhz30t	Indian tiger	Panthera tigris tigris
4	bhz45t	Indian tiger	Panthera tigris tigris
5	bhz56t	Indian tiger	Panthera tigris tigris
6	bhz63t	Indian tiger	Panthera tigris tigris
7	bhz20wt	Indian white tiger	Panthera tigris bengalensis
8	bhz22wt	Indian white tiger	Panthera tigris bengalensis
9	bhz23wt	Indian white tiger	Panthera tigris bengalensis
10	bhz28wt	Indian white tiger	Panthera tigris bengalensis
11	gz11	Normal leopard	Panthera pardus
12	g z 2l	Normal leopard	Panthera pardus
13	gz3l	Normal leopard	Panihera pardus
14	gz21cl	Clouded leopard	Neofelis nebulosa
15	gz22ci	Clouded leopard	Neofelis nebulosa
16	darz14sl	Snow leopard	Panthera unicia
17	darz15sl	Snow leopard	Panthera unicia
18	darz16sl	Snow leopard	Panthera unicia
19	sbz22al	Asiatic lion	Panthera leo persica
20	sbz38al	Asiatic lion	Panthera leo persica
21	sbz39al	Asiatic lion	Panthera leo persica
22	humsk	Human	Homo sapiens sapiens
23	chimss	Chimpanzee	Pan sp.

Table 6. Multiple sequence alignments of the cytochrome b sequences of reference animals with the sequence obtained from confiscated animal remain

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sbz22al	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
s5:38al	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
sbz39al	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCTGACACGATTCTTTGCCTTCCAC TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCTGACACGATTCTTTGCCTTCCAC	60
adil.flesh	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCTTCCAC	60
gzini	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCTTCCACTGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCTTCCAC	60
gz2nl	TGAATCTGAGGAGGCTTCTCAGAGACAAAGCTACCTTGACACGATTCTTTGCCTTCCAC	60
gz3nl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCTTCCAC	60
bh:23wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bh=28wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bh=22wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz20wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC TGAATCTGAGGAGGCTCTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz63t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhzSác	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	63
bhz26t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz30t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bhz45c	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
bh=25t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
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d:15sl	TGAATCTGAGGAGGCTTCTCAGTACACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC TGAATCTGAGGAGGCTTCTCAGTACACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC	60
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gz21cl	TGAATCIGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTTTTCGCCTTCCAC TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTTTTCGCCTTCCAC TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTTTTCGCCTTCCAC	60
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bh=22wt	GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
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bhz25t	GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
dz14sl	GTCCTATTCTCACCAGACCTATTAGGGGACGCCGATAACTACATCCCCGCCAACCCTCTA 300
dz15sl	GTCCTATTCTCACCAGACCTATTAGGGGACGCCGATAACTACATCCCCGCCAACCCTCTA 300
d:16sl	GTCCTATTCTCACCAGACCTATTAGGGGACGCCGATAACTACATCCCCGCCAACCCTCTA 300
gz21cl	GTTCTATTCTCCCCAGACCTACTAGGAGACCCTGACAATTACACTCCCGCCAACCCTCTA 300
g222cl	GTTCTATTCTCCCCAGACCTACTAGGAGACCCTGACAATTACACTCCCGCCAACCCTCTA 300
chimss	ACACTATTCTCACCAGACCTCCTGGGCGATCCAGACAACTATACCCTAGCTAACCCCCTA 300
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Table 7c

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Table 8. Percent simitarity matrix calculated by pair-vise comparisons of cytochrome b gene sequences revealed from 'adil.flesh' and different felids

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	bhz20wt bhz25t	bhz25t	dz14si	humsk	chimss	sbz22al	D21L	gz2L	023L	gz21cl	adil.flesh
bhz20w1		100	99.1	81.7	78.7	93.3	95.1	95.4	95.4	9.68	95.4
bhz25t	100		99.1	81.7	78.7	93.3	95.1	95.4	95.4	9.68	95.4
dz14sl	1.66	99.1		81.4	78.4	93	94.8	95.1	95.1	89.3	95.1
humsk	81.7	81.7	81.4		6.98	79.6	81.1	80.2	80.2	79	81.4
chímss		7.8.7	78.4	86.9		78.7	79.6	78.7	7.8.7	76.8	79.9
sbz22ai	93.3	93.3	. 93	79.6	78.7		92.1	92.4	92.4	89	92.4
gz1L		95.1	94.8	81.1	9.62	92.1	3 1 to 100 to 100 to	98.5	98.5	89.3	7.66
gr2L	95.4	95.4	95.1	80.2	78.7	92.4	98.5	選 選	100	88.1	98.2
graf	95.4	95.4	95.1	80.2	78.7	92.4	98.5	100	; i*	88.1	98.2
9221cl	89.6	9.68	89.3	79	76.8	89	89.3	98.1	88.1		89.6
adil.flesh		95.4	95.1	81.4	79.9	92.4	200.7	98.2	98.2	89.6	

Table 10



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), *Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984591695-10075-13605

Query-

(25 letters)

Database: nt

807,597 sequences: 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAOS

Taxonomy reports

Distribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments	
×	
·	·
•	

E Score (bics) Value Sequences producing significant alignments: 50 2e-05 gb|AF231651.1|AF231651 Strongylura notata clone HB-82 cytoc...
gb|AF231650.1|AF231650 Strongylura notata clone HB-159 cyto... _50 2e-05 _50 2e-05 ref NC 002672.1 Dinornis giganteus mitochondrion, complete...
ref NC 002673.1 Emeus crassus mitochondrion, complete genome <u>5</u>0 2e-05 ref NC 002673.1 Emeus crassus mitochondrion, complete genome 50 2e-05 qb AF232015.1 AF232015 Nothrotheriops shastensis cytochrome. 50 2e-05 qb AF232013.1 AF232013 Bradypus variegatus cytochrome b gen. 50 2e-05 qb AY016015.1 Emeus crassus mitochondrion, complete genome 50 2e-05 qb AY016013.1 Dinornis giganteus mitochondrion, complete g. 50 2e-05 qb AY016014.1 Dromaius novaehollandiae mitochondrion, part. 50 2e-05 qb AY016014.1 Bromaius novaehollandiae mitochondrion, part. 50 2e-05 qb AF074594.1 AF230167 Bonasa umbellus cytochrome b (CYT3) 50 2e-05 qb AF074594.1 AF074594 Baeolophus bicolor cytochrome b gene. 50 2e-05 qb AY005210.1 Poospiza melanoleuca isolate 3 cytochrome b 50 2e-05 qb AY005209.1 Poospiza melanoleuca isolate 2 cytochrome b 50 2e-05 qb AY005208.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 60 cytob 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 60 cytob 50 2e-05 qb AY005205.1 Poospiza melanoleuca isolate 1 cytochrome b 60 cyto gb | AY005203.1 |Poospital hispaniolensis cytochrome b (cytb)502e-05gb | AY005204.1 |Poospital garleppi cytochrome b (cytb) gene.502e-05gb | AY005203.1 |Poospital erythrophrys cytochrome b (cytb) gene.502e-05gb | AY005201.1 |Poospital boliviana cytochrome b (cytb) gene.502e-05gb | AY005199.1 |Poospital alticolal isolate 2 cytochrome b (cytb)502e-05gb | AY005198.1 |Poospital alticolal isolate 1 cytochrome b (cytb)502e-05gb | AF155870.1 |AF155870 |Heterocephalus glaber cytochrome b (cytb)502e-05gb | AF102099.1 |AF102099 |Criniferoides leucogaster cytochrome b (cytb)502e-05gb | AF102095.1 |AF102095Corythaixoides concolor cytochrome b (cytb)502e-05gb | AF271065.1 |AF271065 |Mustelal ermineal specimen - voucher all (cytochrome b)502e-05gb | AF243857.1 |AF243856 |Strongylural notatal notatal cytochrome (cytochrome b)502e-05gb | AF306872.1 |AF306872 |Brachyramphus marmoratus haplotype M (cytb)502e-05gb | AF306871.1 |AF306871 |Brachyramphus marmoratus haplotype M (cytb)502e-05 ref NC 001567.1 Bos taurus mitochondrion, complete genome

b AF306872.1 AF306872

b AF306871.1 AF306871

b AF306870.1 AF306870

b AF306869.1 AF306869

b AF306869.1 AF306868

b AF306868.1 AF306868

c AF248662.1 AF306868

c AF248662.1 AF348661

c AF348661.1 AF348661

c AF348661

c AF348661.1 AF348661

c A 50 2e-05 50 2e-05 50 2e-05 50 2e-05

Table 9. Animals selected for validation of minimum P'S score for efficient amplification of DNA templates in PCR

SL.	Name	P. S/AFF	P. S/AFR	
1	Indian black buck (Antilope cervicapra)	97, 58	96, 54	
2	Sheep (Ovis	87, 53	96, 54	
3	Pig (Sus scrofa)	87, 52	87, 41	
4	Fresh water dolphin (Platanista gangetica)	86, 49	82, 47	

Sequences producing significant alignments:		ore ics)	E Value
gb[AF2]1651.1 AF231651 Strongylura notata clone HB-82 cytoc	50	2e-	05
gb AF231650.1 AF231650 Strongylura notata clone HB-159 Cyto	_50	2e-	
ref[NC 002672.1] Dinornis giganteus mitochondrion, complete	_5.0		
ref[NC 002673.1] Emeus crassus mitochondrion, complete genome	_5.0		
gb AF232015.1 AF232015 Nothrotheriops shastensis cytochrome	_ <u>50</u> 50	2e- 2e-	
gb[AF232013.1]AF232013 Bradypus variegatus cytochrome b gen gb[AY016015.1] Emeus crassus mitochondrion. complete genome	<u></u>	2e-	
gb[AY016015.1] Emeus crassus mitochondrion, complete genome gb[AY016013.1] Dinornis giganteus mitochondrion, complete g	50		
gb AY016014.1 Dromaius novaehollandiae mitochondrion, part	50	2e-	
gb AF230167.1 AF230167 Bonasa umbellus cytochrome b (CYT3)	_50		
gb AF074594.1 AF074594 Baeolophus bicolor cytochrome b gene	<u>50</u>	2e- 2e-	•
gb AY005210.1 Poospiza melanoleuca isolate 3 cytochrome b gb AY005209.1 Poospiza melanoleuca isolate 2 cytochrome b	<u>50</u>	2e-	
<pre>gb AY005209.1 Poospiza melanoleuca isolate 2 cytochrome b gb AY005208.1 Poospiza melanoleuca isolate 1 cytochrome b</pre>	50	2e-	
cb[AY005205.1] Poospiza hispaniolensis cytochrome b (cytb)	50	2e-	
gb[AY005204.1] Poospiza garleppi cytochrome b (cytb) gene	50		
gb[AY005203.1] Poospiza erythrophrys cytochrome b (cytb) ge	<u> 50</u>	2e-	
gb AY005201.1 Poospita boliviana cytochrome b (cytb) genegb AY005199.1 Poospita alticola isolate 2 cytochrome b (cy	<u>50</u> 50		
<pre>qb[AY005199.1] Poospiza alticola isolate 2 cytochrome b (cy qb[AY005198.1] Poospiza alticola isolate 1 cytochrome b (cy</pre>	50		
gb/AF155870.1/AF155870 Heterocephalus glaber cytochrome b (50		25
cb[AF189123.1[AF189123 Glyptotermes eukalypti cytochrome b	50		
gb AF102099.1 AF102099 Criniferoides leucogaster cytochrome	_50	2e-0	
gb AF102095.1 AF102095S1 Corythaixoides concolor cytochrome	<u>50</u>	2e-(
gb/AF271065.1/AF271065 Mustela erminea specimen-voucher AF1 gb/AF243857.1/AF243857 Strongylura notata notata cytochrome	50	20-0	
gb/AF243856.1/AF243856 Strongylura notata forsythia cytochr	50	2e-0	5
refinc 001567.1 Bos taurus mitochondrion, complete genome	50	2e-0	
gb/AF306872.1/AF306872 Brachyramphus marmoratus haplotype M	_50	2e-0	
gb/AF306871.1/AF306871 Brachyramphus marmoratus haplotype M	<u>50</u> 50	2e-0	
gb AF306870_1 AF306870 Brachyramphus brevirostris haplotype	50	2e-0	
gb/AF306868.1/AF306868 Brachyramphus brevirostris haplotype	50	2e-0	15
gb AF010406.1 AF010406 Ovis aries complete mitochondrial ge	50	2e-0	
gb AF248662.1 AF248662 Gryllus campestris haplotype 2 cytoc	<u>50</u>	2e-0	
cb AF248661.1 AF248661 Gryllus campestris haplotype 1 cytoc	<u>50</u>	2e-0	
gb AF096462.1 AF096462 Rhipidura albicollis cytochrome b ge gb AF283644.1 AF283644 Elaphe obsoleta cytochrome b gene, c	50	2e-0	
cblAF283643.1 AF283643 Elaphe obsoleta cytochrome b gene, c	50	2e-0	
gb AF283642.1 AF283642 Elaphe obsoleta cytochrome b gene, c	_50	2e-0	
gb[AF283641.1]AF283641 Elaphe obsoleta cytochrome b gene, c	_ <u>50</u> _50	2e-0	
gb AF283640.1 AF283640 Elaphe obsoleta cytochrome b gene, c gb AF283639.1 AF283639 Elaphe obsoleta cytochrome b gene, c	50	2=-0	
gbiAF283637.11AF283637 Elaphe obsoleta LSUMZ 45359 cytochro	_50	2e-0	
gb[AF283636.1 AF283636 Elaphe obsoleta LSUMZ 44662 cytochro	_50	2e-0	
gb[AF283635.1 AF283635 Elaphe obsoleta LSUMZ 40443 cytochro gb[AF283634.1 AF283634 Elaphe obsoleta LSUMZ 44335 cytochro	<u>50</u>	2e-0	
gb[AFZ83634.1[AFZ83634 Elaphe obsoleta LSUMZ 44335 cytochro gb[AFZ83633.1[AFZ8363] Elaphe obsoleta LSUMZ 42624 cytochro	50	2=-0	
qb/AF283632.1/AF283632 Elaphe obsoleta LSUME H1911 cytochro	50	2=-0	
gb AF283631.1 AF283631 Elaphe obsoleta LSUMZ 41197 cytochro	<u>50</u> 50	2e-0 2e-0	
gb AF283630.1 AF283630 Elaphe obsoleta LSUMZ 41189 cytochro gb AF283629.1 AF283629 Elaphe obsoleta LSUMZ 41188 cytochro	50	2=-0	
gb AF283628.1 AF283628 Elaphe obsoleta LSUMZ 41187 cytochro	50	20-0	
gb/AF283627.1 AF283627 Elaphe obsoleta LSUME 41186 cytochro	_50	2e-0	
gb AF283626.1 AF283626 Elaphe obsoleta LSUMZ 40943 cytochro gb AF283625.1 AF283625 Elaphe obsoleta LSUMZ 37499 cytochro	_ <u>50</u>	20-0	5
qb AF283625.1 AF283625 Elaphe obsoleta LSUMZ 17499 cytochro qb AF283624.1 AF283624 Elaphe obsoleta LSUMZ 44480 cytochro	50	2=-0	S
qb[AF283623.1]AF283623 Elaphe obsoleta LSUME 44451 cytochro	50	24-0	
gb[AF28]622.1[AF28]622 Elaphe obsoleta LSUM2 40444 cytochro	<u>_50</u>	2e-0:	
gb AF28]621.1 AF28]621 Elaphe obsoleta LSUMZ 19925 cytochro gb AF28]620.1 AF28]620 Elaphe obsoleta LSUMZ 19161 cytochro	<u>50</u> <u>50</u>	2e-0	5
chiAF283619.1[AF283619 Elaphe obsoleta LSUM239162 cytochrom	_50	201	5
gbiAF283618.11AF283618 Elaphe obsoleta LSUMZ H15836 cytochr	_50	Ze -01	
dbiaF283615_liaF281617 Elaphe obsoleta LSUME His832 cytochr dbiaF283616_liaF281616 Elaphe obsoleta LSUME 15831 cytochro	<u>50</u> -50	2e-0	
db AF283615.1 AF283615 Elaphe obsoleta LSUME HLS870 cytochr	23	2=-0	
ablaf293614 11AF283614 Elaphe obeoleta LSUME H15887 cytochr	57	3=-03	;
qb[AF78]61] 1[AF78]61] Elaphe obsoleta LSUM2 H15888 cycoche	27	2=-01	,

gb[AF283612.1]AF283612	Elaphe obsoleta LSUMZ H15884 cytochr	50	2e-05
qh[AF283611.1[AF283611	attach checlera LSUME H15031 Cytochr	50	2e-05
<u>40 AF 283611 . 1 AF 283610</u>	at the checkers LSUMI HISOID CYCOCHI	_50	2e-05
gb AF283610.1 AF283610 gb AF283609.1 AF283609	minha obsoleta CAS 169468 CYCOCATOM	50	2e-05
gb[AF283608.1]AF283608	Elante chacleta LSUMI H14781 Cytocht	_50	2e-05
GETAF 28 3 608 . 1 1 AF 28 3 60 7	Flanks chapleta LSUME H14781 Cytoche	_50	2e-05
95 AF28 1607 . 1 AF28 3607	Flanke charleta LSUME H14724 Cytochi	50	2e-05
gb AF283606.1 AF283606	Flanks obsoleta cytochrome b gene. C	_50	2e-05
gb AF283605.1 AF283605	Flanke chapleta cytochrome b gene, C	50	2e-05
gb AF283604 . 1 AF283604	Flanka obsoleta cytochrome b gene, C	50	2e-05
gb AF283603.1 AF283603	Elaphe obsoleta LSUME H3388 cytochro	50	2e-05
95 AF283602.1 AF283602	Elaphe obsoleta LSUMZ H3385 cytochro	50	2e-05
95 AF283601.1 AF283601	Flanks obsoleta LSUMZ H3384 Cytochro	_50	2e-05
gb AF283600.1 AF283600	Flanke bairdi LSUME H3382 cytochrome	_50	2e-05
gb AF283599.1 AF283599	Flanke hairdi LSUMZ H3381 cytochrome	_50	2e-05
gb AF283598 . 1 AF283598	Flanks obsoleta LSUMZ H3379 Cytochio	_50	2e-05
gb AF283597.1 AF283597	Flanke obsoleta LSUMZ 39616 Cytochro	_50	2e-05
cb AF283596.1 AF283596	Flanke obsoleta LSUMZ H3376 cytochro	_50	2e-05
95 AF283595.1 AF283595	Flanke obsolera LSUMZ H3345 Cytochio	_50	2e-05
gb AF283594.1 AF283594	Flanke obsoleta LSUMZ H3309 CytoGRIO	50	2e-05
gb AF283593.1 AF283593	Flance obsoleta LSUMZ H3306 Cytochio	_50	2e-05
GB AF283592.1 AF283592	Flanke obsoleta LSUMZ H3276 Cytochio	_50	2e-05
gb AF283591.1 AF283591 gb AF283590.1 AF283590	Flanka obsoleta LSUMZ H3246 Cytochio	<u> 50</u>	2e-05
95 AF 28 35 90 . 1 AF 28 35 89	Flanke obsoleta LSUMZ H3212 Cytochro	<u>50</u>	2e-05
gb AF283589.1 AF283589 gb AF283588.1 AF283588	Flanke obsoleta LSUMZ H3209 Cytochio	_50	2e-05
CD AF283588.1 AF283587	Flanke obsoleta LSUMZ H3206 CYtocaro	_50	2e-05
GD AF283587.1 AF283587 GD AF283586.1 AF283586	Flanke chapleta LSUMZ H3191 Cytochio	_50	2e-05
GD AF283585.1 AF283585	Flance obsoleta LSUMZ H3190 cytochro	_50	2e-05
GD AF283584 . 1 AF283584	Flance obsoleta LSUMZ H3189 cytochro	_50	2e-05
cb AF283583.1 AF283583	Flance obsoleta LSUMZ H3188 Cytocaro	_50	2e-05
gb AF283582.1 AF283582	Flanke obsoleta LSUMZ H3186 Cytochio	_50	2e-05 2e-05
CD AF283581 . 1 AF283581	Flance obsoleta LSUMZ H3169 CytochEc	50	2e-05
GD AF283580 . 1 AF283580	Flanke obsoleta CAS 203083 Cytocarom	50	2e-05
gb AF283579.1 AF283579	Flanks obsoleta CAS 203079 Cytochiom	<u> 50</u>	2e-05
GD AF283578.1 AF283578	elamba obsoleta LSUMZ H2286 Cytochio	<u> 50</u>	2e-05
GD AF283577.1 AF283577	Flance obsoleta CAS 208631 cycochrom	<u> 50</u>	2e-05
Gb AF283576.1 AF283576	Elaphe obsoleta LSUMZ H2229 cytochro	50	2e-05
GD AF187030 . 1 AF187030	Rhinophylla pumilio isolate TX46001	50	2e-05
GD AF310052.1 AF310052	Poospira hispaneolensis cytochrome b	50	2e-05
gb AF310046.1 AF310046	Volatinia jacarina cytochrome b gene Deinagkistroden acutus cytochrome b	50	2e-05
gb AF171919.1 AF171919	Trimeresurus mucrosquamatus cyth gen	50	2e-05
GD AF171897.1 AF171897	Agelaius cyanopus cytochrome b (cytb	50	2e-05
GD AF290174 . 1 AF290174	Agelaius phoeniceus cytochrome b (cy	50	2e-05
GD AF290173.1 AF290173	Quiscalus major cytochrome b (cytb)	50	2e-05
gb AF290171.1 AF290171 gb AF290170.1 AF290170	Ashimermia holosericeus cytochiome	<u> 50</u>	2e-05
gb AF290150.1 AF290150	volarinia jacarina cytochrome b (cyt	50	2e-05
95 AF176252.1 AF176252	pairbrodontomys zacatecae cytochrome	50	2e-05 2e-05
95 AF176251.1 AF176251	pairbrodogromys zacatecae cytochrome	<u>50</u>	2e-05
95 AF163907.1 AF163907	wiczonia wanthognathus cytochiome D	<u>50</u> 50	2e-05
GD AF163904.1 AF163904	Microtus pinetorum cytochrome b gene	50	2e-05
gb AF163901.1 AF163901	Microtus ochrogaster cytochrome b ge	50	Ze-05
gb AF163899.1 AF163899	Microtus miurus cytochrome b gene. c Microtus californicus cytochrome 8 (50	2e-05
gb AF163891.1 AF163891	Microtus abbreviatus cytochrome B (c	50	2e-05
gb AF163890.1 AF163890	Dipsochelys dussumieri isolate Germa	5.7	Ze-05
GD AF288524 . 1 AF288524	nimochalva dussumieri isolate White	50	2e-05
gb AF288523.1 AF288523 gb AF288522.1 AF288522	nimentalva dussumieri isolate ALCY	50	2e-05
95 AF123530 . 1 AF123530	neilonged pyrolophus cytochrome b (50	2e-05 2e-05
95 AF123512.1 AF123512	Enhacea hourgierii tuginkae cytochio	50	2e-05
GD AF206548 . 1 AF206548	Admitus vautregelli cytochrome D 985	<u>50</u>	2e-05
gb AF197857. 1 AF197857	Cymnorhina tibicen cytochrome b gene	50	20-05
95 [U6] 397.2 SEU6] 397 S	itta europaea cytochrome b gene, part	50	Ze-05
== 1NC 001945.11 Dinod	on semicarinatus mitochondrion, compl us novemcinctus mitochondrion, comple	50	Ze-05
TELINC OGIBEL. LI Dasyp	Daeymye incomtus country Tanzania cy	5.7	2e-05
95 AF141217. 1 AF141217	negodon huchholai cyotchrome b gene	50	Ze-05
gb AF201615,1 AF201615 gb AF077920,1 AF077920	annhus nevadensis cycochrome b gene	750	Ze-05
	Organica americanus cytochrome b (cy	57	Ze-05 Ze-05
95 J01 194 1 1 80 WT 80 8	remain mirochondrion, complete genome	50	26-05
951AF191810.11AF191810	Cochlearius cochlearius cytochrome b	22	/

PCT/IN01/00055

gt/U69181.1 CAU69181 Chlorostilbon aureoventris cytochrome	50	24-05
gb U89171.1 AFU89171 Asio flammeus cytochrome b (cytb) gene	50	26-05
	50	
	50	
gb AF217822.1 AF217822 Hydrophis semperi cycochrome b gene		
qb AF217813.1 AF217813 Acanthophis antarcticus cytochrome b	_50	
gb[AF220408.1]AF220408 Calliophis kelloggi cytochrome b (cy	_5.0	
gb[AF126430.1[AF126430 Ellobius fuscocapillus cytochrome b	50	2e-05
gb/AF090337.1/AF090337 Aythya americana mitochondrion. comp	<u>_50</u>	2e-05
gb[AF059111.1 AF059111 Sarkidiornis melanotos cytochrome b	_50	2e-05
gb[AF059053.1 AF059053 Aix sponsa cytochrome b gene, partia	50	2e-05
gb AF099308.1 AF099308 Icterus wagleri wagleri cytochrome b	5.0	2e-05
	50	2e-05
	_50	2e-05
gb AF099294.1 AF099294 Icterus gularis tamaulipensis cytoch		2e-05
gb/AF099293.1 AF099293 Icterus gularis gularis cytochrome b	_50	
gb AF160610.1 AF160610 Cricetomys emini Cemi636 cytochrome	50	2e-05
gb AF036280.1 AF036280 Tragelaphus strepsiceros cytochrome	_50	2e-05
gb[AF036277.1]AF036277 Tragelaphus scriptus cytochrome b (c	_50	
<pre>gb[AF036274.1] Tetracerus quadricornis cytochrome b (cytb)</pre>	_50	2e-05
qb AF194218.1 AF194218 Phrynosoma platyrhinos cytochrome b	<u>_so</u>	2e-05
gb/AF194216.1/AF194216 Urosaurus ornatus cytochrome b gene,	50	2e-05
ref NC 002009.1 Artibeus jamaicensis mitochondrion, comple	_50	2e-05
ref NC 001941.1 Ovis aries mitochondrion, complete genome	50	2e-05
ref[NC 000877.1] Aythya americana mitochondrion, complete g	50	2e-05
	50	2e-05
	50	2e-05
gb/U27551.1 GCU27551 Grus canadensis tabida cytochrome b (c	50	2e-05
gb[AF089058.1]AF089058 Quiscalus quiscula cytochrome b (cyt	50	2e-05
gb[AF089055.1]AF089055 Quiscalus major cytochrome b (cytb)		2e-05
gb AF089054.1 AF089054 Quiscalus lugubris cytochrome b (cyt	<u>50</u>	2e-05
gb[AF089046.1]AF089046 Oreopsar bolivianus cytochrome b (cy	_50	
cb AF089042.1 AF089042 Molochrus badius cytochrome b (cytb)	50	2e-05
gb AF089039.1 AF089039 Macroagelaius imthurmi cytochrome b	_50	2e-05
GD AF089037.1 AF089037 Lampropsar tanagrinus cytochrome b (<u> 50</u>	2e-05
cb/AF089026.1/AF089026 Gymnomystax mexicanus cytochrome b (_50	2e-05
gb/AF089025.1/AF089025 Gnorimopsar chopi cytochrome b (cytb	50	2e-05
cb AF089024.1 AF089024 Euphagus cyanocephalus cytochrome b	50	2e-05
cb AF089023.1 AF089023 Euphagus carolinus cytochrome b (cyt	50	2e-05
cb AF089021.1 AF089021 Dives warszwewiczi cytochrome b (cyt	50	2e-05
cb AF089020.1 AF089020 Curaeus curaeus cytochrome b (cyto)	50	2e-05
gb AF089016.1 AF089016 Amblycercus holosericeus cytochrome	_50	2e-05
gb(AF089013.1/AF089013 Agelaius xanthophthalmus cytochrome	50	2e-05
gb AF089012.1 AF089012 Agelaius xanthomus cytochrome b (cyt	50	2e-05
gb AF089008.1 AF089008 Agelaius phoeniceus sub-species phoe	50	2e-05
gb AF069006.1 AF089006 . Agelaius humeralis cytochrome b (cyt	50	2e-05
cb/AF089005.1/AF089005 Agelaius cyanopus cytochrome b (cytb	50	2e-05
cb AF108696.1 AF108696 Scolomys juruaense cytochrome B (cyt	50	2e-05
gb AF108685.1 AF108685 Wiedomys pyrrhorhinos cytochrome B (50	2e-05
cb/AF108677.1/AF108677 Thomasomys oreas cytochrome B (cyt3)	50	2e-05
cb AF145511.1 AF145511 Melanoplus foedus cytochrome b gene	50	2e-05
gb AF145511.1 AF145511 Melanoplus angustipennis cytochrome	50	2e-05
gb U89627.1 BMU89627 Bolicoglossa marmorea cytochrome b (cy	50	2e-05
q5/089623.1 8PU89623 Barrachoseps pacificus cycochrome b (c	50	2=-05
q5 AF181470.1 AF181470 Okapia johnstoni cytochrome b gene,	50	2e-05
qb[AF084075.1[AF084075 Lagenorhymchus acutus cytochrome b g	50	2e-05
q5[490303.1[0M49030] Ovibos moschaeus cycochrome 5 (cycb) g	50	2=-05
ab U90302.1 OMU90302 Ovibos moschatus cytochrome b (cytb) g	50	2e-05
q5 U90301.1 OMU90301 Ovibos moschatus cytochrome b (cytb) g	50	2e-05
q5 U90300.1 OMU90300 Ovibos moschazus cytochrome b (cytb) g	50	Ze-05
gb[AF038883.1[AF03888] Deinagkistrodon acutus cytochrome b	50	2 - -05
gb AF039268.1 AF039268 Agkistrodon contortrix cytochrome b	50	2=-05
gb[AF039267.1[AF039267 Boa constrictor cytochrome b (cytb)	50	Z=-05
gb[549215.1[549215 apocytochrome b (sheep, domestic, Merino	50	2=-05
gbiAF158698.1 AF158698 Geomys pinetis Cytochrome b gene. co	50	2e-05
gb AF158692.1 AF158692 Geomys bursarius jugossicularis cyto	50	Ze-05
gb[AF068193.1[AF068193] Ithaginis cruentus cytochrome b (cyt	50	2e-05
qb[AF091629.1]AF091629 Ancilocapra americana Cytochrome b (50	2=-05
qb[AF02206] .1] Tragelaphus screpsiceros cytochrome b (cytb)	50	20-05
gb[AF022062.1] Tragelaphue derbianue cytochrome b (cytb) ge	_3_7	25-05
qb[AF022060 1] Hippocraque equinus cytochrome b (cytb) gene	57	15-03
qb[AF023057.1] Tragelaphus oryx cytochrome b (cyto) gene, m.	50	22-05
golAFILISOO ILAFLISOO Lagenorhynchus acutus Laciate LACU74	-57	205
gb[AF11]499 1[AF11]499 Lagenorhymchus acutus Laciate (ACIA) .	<u> </u>	25.05

gb Uc4645.1 LBUc4645 Loxocemus bicolor cycochrome b (cycb)	50	2e-05
Thinke to themseath Funeries notaeus cytochrome b (cytb) 9	_50	2e-05
Therefore a least GAGE Fundames murious eviochrome b (cytb) 9	_5 <u>0</u>	2e-05
This can alreas and Friends strictus fosteri CytoChrome	.50	2e-05
Turner of property Friends Striatus Strigilatus CytoChr	_50	2e-05
Throng throught Enigrapes strictus strictlatus cytocat	_50	2e-05
This can alreason Friends Striatus mocraniel Cycochiom	_50	2e-05
This care a legislated Enionated Striatus modfaniel Cytochrom	_50	2e-05
Tricages to chicages moners; s cytochrome b (cyto)	<u> 50</u>	2e-05 2e-05
The same of the court of the co	50	2e-05 2e-05
ablu69786.11EFU69786 Epicrates ford: cytochrome B (2975)	<u> 50</u>	2e-05
The second of th	<u>50</u> 50	2e-05
gb[U69779.1[ECU69779 Epicrates Centhria Cytochrome b (Gyrb)	50	2e-05
gb U69779.1 ECU69777 gb U69777.1 ECU69777 Epicrates cenchria cytochrome b (cytb)	50	2e-05
gb U69777.1[ECU69777 gb U69776.1[EAU69776 Epicrates angulifer cytochrome b (cytb gb U69774.1[EAU69774 Epicrates angulifer cytochrome b (cytb	50	2e-05
	50	2e-05
cb U69772.1 CEU69772 Corallus enveris cytochrome b (cyto) g cb U69771.1 CEU69771 Corallus enveris cytochrome b (cyto) g	50	2e-05
	50	2e-05
	50	2e-05
Candoja aspera cytochrome b (cyto) gen	50	2e-05
The state of the constrict of cytopies by (cyto) 98	_50	2e-05
increase the micros and constrictor eventhrome b (cyta) ge	_50	2e-05
The same of the sa	_50	2e-05
blamanaga Tlamanaga Phea americana mitochondrion, comple	_50	2e-Q5
The same all socials Chemidophorus tigris strain Isla Ang	_50	2e-05
Lineager ilamanere Chemidophorus tigris strain ista omi	<u> 50</u>	2e-05 2e-05
cb AF034969 1 AF034969 Connochaetes taufinus cytochisme 2 9	<u>50</u>	2e-05
cb/AF028822.1/AF028822 Alcelaphus Buselaphus Cytochionic	50	2e-05
GD AF028821.1 AF028821 Damaliscus Tunatus Cytochrome Julia	50	2e-05
	50	2e-05
	50	2e-05
	50	2e-05
illegacoca illegacoca Oceanodicma furcata cytochrome b (cy	_50	2e-05
the parents the parents that the parents of the par	_50	2e-05
largaces ilargaces Garrodia nereis cytochrome b (cytb)	_50	2e-05
Transpara : largarea : regerra tropica cytochrome b (cytb)	_50	2e-05 2e-05
blancacos ilaporcoso injumedea gibsoni cytochrome b (cytb)	<u>50</u>	2e-05
gb AF076049.1 AF076049 Diomedea epomophora cycochrome D (c)	50	2e-05
GDIAF076049.1 AF076048 Diomedea Chionoptera Cytochione D	50	2e-05
	50	2e-05
gb UE3314.1 MSU83314 Micrastur semitorquatus cytochrome b (75-07
	50	2e-05
gb U83318.1 MEU83318 Microhierax erythrogenys cytochrome b	_ <u>50</u> _50	2e-05 2e-05
cb/US3318.1/MEU83318 Microhierax erythrogenys cytochrome b cb/UJ7303.1/SAU37303 Synthliboramphus antiquus cytochrome b	50 50	2e-05 2e-05 2e-05
cb US3318.1 MEU83318 Microhierax erythrogenys cytochrome b cb U37303.1 SAU37303 Synthliboramphus antiquus cytochrome b cb U37302.1 PAU37302 Ptychoramphus aleuticus cytochrome b	50 50 50	2e-05 2e-05 2e-05 2e-05
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db U83318.1 MEU83318 db U37303.1 SAU37303 gb U37302.1 PAU37302 db U37296.1 CPU37296 gb U37296.1 BBU37289 gb U37289.1 BBU37289 db U37289.1 BBU37289 dephysion of the state of t	50 50 50 50	2e-05 2e-05 2e-05 2e-05 2e-05 2e-05
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db U37303.1 SAU37301 gb U37302.1 PAU37302 gb U37296.1 CPU37296 gb U37289.1 B3U37289 gb U37286.1 APU37286 Aethia pygmaea cytochrome b gene, mito gb U37104.1 APU37104 gb U37037.1 ACU37087 gb U37525.1 HGU87525 Aethia cristatella cytochrome b gene gb U37524.1 HGU87524 Heterocephalus glaber cytochrome b gen	50 50 50 50 50 50 50 50 50	2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05
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Microhierax erythrogenys cytochrome b cb U37303.1 SAU37301 gb U37302.1 PAU37302 cb U37296.1 CPU37296 cb U37289.1 BBU37289 gb U37286.1 APU37286 cb U37206.1 APU37286 cb U37206.1 APU37286 cb U37104.1 APU37104 cb U37087.1 ACU37087 cb U37087.1 ACU37087 cb U37525.1 HGU87525 cb U87523.1 HGU87524 cb U87523.1 HGU87524 cb U37524.1 HGU87524 cb U37524.1 HGU87524 cb U3764.1 STU37664 cb U37664.1 STU37664 cc U37666.1 CPU37664 cc U37666.1 CPU37664 cc U37666.1 CPU37664 cc U37666.1 CPU37664 cc U37666.1 CPU376664 cc U376666.1 CPU376664 cc U376666.1 CPU376664 cc U37666666666666666666666666666666666666	50 50 50 50 50 50 50 50 50 50 50 50 50 5	2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05
### Microhierax erythrogenys cytochrome b ### Synthliboramphus antiquus cytochrome b ### Cyclorrhynchus psittacula cytochrome b gene, mito ### Cyclorrhynchus psittacula cytochrome	50 50 50 50 50 50 50 50 50 50 50 50 50 5	2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05 2e-05
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db U37303.1 SAU37303 gb U37302.1 PAU37302 gb U37296.1 CPU37296 gb U37289.1 SBU37289 gb U37286.1 APU37286 gb U37104.1 APU37104 Aethia pygmaea cytochrome b gene, mito. gb U37037.1 ACU37087 gb U37525.1 HGU87525 gb U87525.1 HGU87525 gb U87525.1 HGU87525 gb U87525.1 HGU87525 gb U87525.1 HGU87526 gb U3754.1 HGU87527 gb U87525.1 HGU87527 gb U87526.1 HGU87527 gb U87526.1 HGU87527 gb U87526.1 HGU87527 gb U37526.1 I GU87527 gb U37526.1 I GU87527 gb U37526.1 I GU87527 gb U37863.1 I GAU17864 gb U37862.1 OMU17862 gb U37862.1 OMU17862 gb U37862.1 I GU37862 gb U37862	50 50 50 50 50 50 50 50 50 50 50 50 50 5	2e-05 2e
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db U37303.1 SAU37303 gb U37302.1 PAU37302 gb U37296.1 CPU37296 gb U37289.1 BBU37289 gb U37286.1 APU37286 gb U37286.1 APU37286 gb U37104.1 APU37104 Aethia pygmaea cytochrome b gene, mito gb U37087.1 ACU37087 Aethia pusilla cytochrome b gene, mito gb U37525.1 HGU87525 gb U87525.1 HGU87525 gb U87522.1 HGU87525 gb U87523.1 HGU87525 gb U37524.1 HGU87522 gb U37524.1 HGU87522 gb U37523.1 HGU87523 gb U37523.1 HGU87522 gb U37863.1 OAU17863 oreamnos americanus cytochrome b gene. gb U37863.1 OAU17863 gb U37863.1 OAU17863 gb U37863.1 TBU65264 gb U35263.1 TBU65265 gb U65263.1 TBU65265 gb U65260.1 TBU65265 gb U65260.1 TBU65260 Thomomys bottae cytochrome b (cytb) ge	50 50 50 50 50 50 50 50 50 50 50 50 50 5	2e-05 2e
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cblu3318.1 MEU8318 cblu37303.1 SAU37303 cblu37302.1 PAU37302 cblu37302.1 PAU37302 cblu37296.1 CPU37296 cblu37289.1 B3U37289 cblu37286.1 APU37286 chlu37286.1 CAPU3786 chlu37286.1 CAPU3	50 50 50 50 50 50 50 50 50 50 50 50 50 5	2e-05 2e
db U83318.1 MEU83318 Microhierax erythrogenys cytochrome b Chiury 103.1 SAU37303 Synthliboramphus antiquus cytochrome b Chiury 103.1 SAU37303 Ptychoramphus antiquus cytochrome b Chiury 103.1 Chiury 103.1 Chiury 103.1 Synthliboramphus antiquus cytochrome b Chiury 103.1 Synthliboramphus antiquus cytochrome b Chiury 103.1 Synthliboramphus aleuticus cytochrome b Chiury 103.1 Sau37289 Sarchytamphus brevirostris cytochrome b Chiury 103.1 Sau37289 Sauchtia pusilla cytochrome b Gene. Chiury 103.1 Suu 103.1 Su	50 50 50 50 50 50 50 50 50 50 50 50 50 5	2e-05 2e
db U83318.1 MEU83318 Microhierax erythrogenys cytochrome b Child U27303.1 SAU37303 Synthliboramphus antiquus cytochrome b Child Child		2e-05 2e
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gb[AF03472F.1] Ovis dall: dall: dytochrome 5 (dyth) gene. m	50	2e-05
gb[AF03472F.1] Ovis dall: call: cytochrome b (cyto) gene gb[AF034727.1] Ovis ammon darwini cytochrome b (cytb) gene	_50	2e-05
gh[AF034717.1] Ovis ammon darwini cytochrome 5 (cyto) generating gh[AF034714.1]AF034724 Pantholops hodgsoni cytochrome b (cyto)	_50	2e-05
db[AF057132.1[AF057132 Taxides taxus cytochrome b (cytb) ge	.50	2e-05
	<u>_50</u>	2e-05
	_50	20-05
	_50	2e-05
	_50	2e-05
	<u> </u>	2e-05
	_5_0	2e-05
gb[AF0062]8.1[AF0062]8 Lamprospiza melanoleuca cytochrome b gb[AF0062]4.1[AF0062]4 Hemispingus acropileus cytochrome b	<u>50</u>	2e-05
gb AF005226_1 AF006226 Cypsnagra hirundinacea cytochrome b	_50	2e-05
gb[AF006215.1]AF006215 Chlorophanes spiza cytochrome b (cyt	_50	2e-05
chlorochrysa calliparaea cytochrome	50	2e-05
Calochaetes coccineus cytochrome b (_50	2e-05
This constant liaron6712 Buthraupis montana cytochrome b (cyt	_50	2e-05
The thought a 1 pourgasta Rupicapra rupicapra rupicapra mito	_50	2e-05
Chiragalis 1/200703415 Rupicapra pyrenaica pyrenaica mito	_50	2e-05
The Taggits 1/DDV203415 Runicabra pyrenaica parva mitochon	_50	2e-05 2e-05
Tagaria il payagala Rupicapra pyrenaica ornata mitocho	<u> 50</u>	2e-05
. I renalis ilemmentato Punicanta funicanta iupicanta meto	_ <u>50</u> 50	2e-05
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to tooking ilumitation underchates pelacicus mitochionumant	_50	2e-05
emb/Y15695.1/SMY15695 Schilbe myscus mitognondrial tyth gain	50	2e-05
embly15697.1 EDY15697 Eutropius depressifostris mitachondri	50	2e-05
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	_50	2e-05
Transpara il programa de la companya nova e hollandia e cytochrome b	_50	2e-05
Clerhrienomys glareolus micochoner	_50	2e-05
threating throwgales Pelecanus onocrotalus cytochrome B gen	<u> 50</u>	2e-05 2e-05
Liveries algoreties pelecanus onociotalus cytochiome B gen	<u>50</u>	26-05
cb U83156.1 AAU83156 Anhinga anhinga cytochrome a gene, mil	50	2e-05
gb/U83155.1/AAU83155 Anhinga anhinga cytochrome B gene, mit	50	2e-05
gb U83154.1 AAU83154 Anhinga anhinga cytochrome B gene, mit gb U81356.1 CLU81356 Chelodina longicollis cytochrome b gen	50	2e-05
	50	2e-05
	_50	2e-05
Timbe longistima mitochondrial Fa	<u>50</u>	2e-05
	_50	2e-05
Transport Desymps novemcingtus complete mitoch	50	2e-05 2e-05
Nemacheilus barbarulus michondria	_ <u>50</u> _50	2e-05
emb[AJ]88468.11IME368468 Ictalurus melas mitchondrial Cyc D.	<u>50</u>	2e-05
emb AJ388459.1 LDE388459 Leucaspius delineatus mittellomatus	50	2e-05
	50	2e-05
	50	2e-05
This Tracera 1 Propressing Furronius depressinostris partial	_50	20-05
This Tracert 11 morrase77 Entropius depressirostris partial	_50	20-05
This Tracers 1/505745676 Eutropius depressirostris partial	<u>50</u>	2e-05 2e-05
This takeers timperassis furgooius depressisosis partial	_ <u>50</u>	2=-05
emb[AJ245674_1]EDE245674 Eucropius depressirostria partiti	50	2e-05
emb Y15884.3 MTRACOMPL Rhea americana complete mitochondria ab U60768.1 PCU60768 Parus cinctus cycochrome b gene, mitoc	50	Ze-05
	50	2e-05
Thirtings Ilmovages Thalassarche chrysostoma cytochrome 5	50	20-05
The same of the sa	50	2e-05 2e-05
	<u>50</u>	2=-05
	50	20-05
gb u4894: 1 Mcue8941 Macronectes grganteus cytochrome b (57	50	205
	50	2=-05
This again throws again and a standard and the control of the cont	50	24-05
	<u> </u>	2=-05
luccena ilaquecena A cheus planicostria cytochrome b (cy	<u> 57</u>	2=-05 2=-05
dplacesot rivoresot verpene opacarae chroqueme p (ches)	-20 -20	7e - 05
aplussion (Actibeus obscurus cytochrome b (cyto)		

		2e-05
gb[U66505.1]ALU66505 Artibeus lituracus cytochrome b (cytb)	ج (ر	2e-05
THE ESTA 1 LETHERENA LANGUAGE TAMALCERSIS CYCOCHIOME O TETTE	50	26-05
THEREAD THE THE CENT BUT THE TAMALCERS IS CVIOCHTOME B (CYT	50	26-03
Thiseen liatureen their intermedius cytochrome D loye	50	2e-05
qb[U66501.1]AIU66501 Arribeus inopinatus cytochrome b (cytb	<u>.5</u> 0	2e-05
	5 Û	2e-05
	50	20-05
gb U63060.1 BBU63060 Brachyramphus brevirostris cycochrome	50	20-05
gb[U63059.1 B8U63059 Brachyramphus brevirostris cytochrome	50	2e-05
gb/u63058.1 BBU63058 Brachyramphus breviroseris cycochrome	50	2e-05
gb[U58]86_1[\$JU58386 Scolomys]uruaense cycochrome b (cyc-b)	_50	2e-05
It is and i I COVMTCVTOD Charloceomys gymnutus mitochoneria.	50	2e-05
gb U34672_1 MNU34672 Merachirus nudicaudatus cytochrome b 1	.50	2e-05
gb U34671.1 MNU34671 Metachirus nudicaudatus cytochrome b 1		2e-05
	_50	20-05
LIVE AS TO I IMPORT CARRECTUS CARRECTUS MICOGRAPICAL CYC	<u>50</u>	2e-05
This and il Covertored Crategeomys tylorhinus mitochondiat	. <u>5</u> 0	2e-05
Thirtians significant Common bursarius juggosicularis mico	_50	2e-05
1711004 11COVMTOVERO CERFOCECONS COLUMNIA GOLUMNIA MILUCIIII	_50	2e-05
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	_50	2e-05
This area 1120146769 Anthus berthelotii cytochrome b gene,	_50	2e-05
The liver of the state of the s	_50	2e-05
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	_50	2e-05
IVASTAT I INCRIMCU N Criseus mitochondrial cytochrome b gene	_50	2e-05
The care always of the mitochondrial cyth gene	_50	Ze-05
ambly86754 1 MTI COVITY L. crumeniferus mitochondrial cyth gene	_50	2e-05
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" : 12275242 1122025242 Partodon buchholzi mitochondriai Cy	_50	2e-05
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la Topogra 1 MIMSCVB22 Dama dama mitochondrial cyth gene	50	2e-05
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orbin Topogra limitorcyB24 Capreolus capreolus mitochondrial	<u> 50</u>	2e-05
THIVOCE A LIMITARY BOS FAUTUS COMPLETE MITOCHORDIAL GENOME	<u> 50</u>	2e-05
ambive some ilminaciona a americana mitochondrion cyth gene	<u> 50</u>	2e-05
This age a larimorum archeus lituratus mitochondrial cyto	<u>50</u> 50	2e-05
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db] AB021093.1 AB021093 Cervus nippon nippon mitochondrial	50	2e-05
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gb L28937.1 CDECY3 Chiroderma doriae cycochrome b gene, b end emb AJ010056.1 CPY010056 Capra pyrenaica (individual 12) mi	<u>_50</u>	2e-05
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emb AJ010053.1 CPY010053 Capra pyrenaida (incividual 10, mar	50	2e-05
emb[AJ010052.1 CPY010052 Capra pyrenaica (individual 9) mit	50	2e-05
Till an age 1 / chunings Canna byrenaica (inglyiqudi 9/ """""""""""""""""""""""""""""""""""	50	2e-05
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- 1. Tologo 2 1 (Cayologe Canta pyrenaica (individual 5) mic	<u>_5</u> 3	2e-05
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ilamana ilamana alces eviochrome b (cytb) gene	43	8e-05
	<u>45</u>	3e-04
40 114 03 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	45	3e-04
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	4.5	3e-04
	4.5	3e-04
	45	3e-04
	46	3e-04
GD[AF157460.1[AF157460] Lepus europaeus cytochrome b (Cyb) g	46	3e-04
GD AF731664.1 AF731664 Tylosurus crocodilus cyco	45	3e-04
cb/AF231663.1/AF231663 Tylosurus crocodilus cione STRI-3537	45	3e-04
golAF231652.1 AF231662 Tylosurus crocodilus Cione Ha-155 Cy	45	3e-04
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Alignments

tmpseq_0	1	taccatgaggacaaatatcattctg	25
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AF231650	398		422
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AY016015	15552		15576
AY016013	15560		15584
AY016014	11516		11540
AF230167	266		290
AF074594	206		230
AY005210	290		314
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AF102095	208		232 422
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AF306872	302		326
AF306871	302		326
AF306870	302 302		326
AF306869	302		326
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AF096462	264		288
AF283644	374		398
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AF203623	374		398
AF201622	374		798
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AF283619	374		398
AF281618	374	******	398
AF283617	374		398
AF283616	374		398
AF283615	374		398
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AF283614	374		398
AF283613	_		398
AF283612	374		398
<u>AF283611</u>	374		398
AF283610	374	• • • • • • • • • • • • • • • • • • • •	
<u>AF283609</u>	374	• • • • • • • • • • • • • • • • • • • •	398
AF283608	374	• • • • • • • • • • • • • • • • • • • •	398
AF283607	374	• • • • • • • • • • • • • • • • • • • •	398
<u>AF283606</u>	374	• • • • • • • • • • • • • • • • • • • •	398
AF283605	374		398
AF283604	374	• • • • • • • • • • • • • • • • • • • •	398
AF283603	374		398
AF283602	374		398
AF283601	374	• • • • • • • • • • • • • • • • • • • •	398
AF283600	374		398
AF283599	374	• • • • • • • • • • • • • • • • • • • •	398
AF283598	374	• • • • • • • • • • • • • • • • • • • •	398
AF283597	374	• • • • • • • • • • • • • • • • • • • •	398
AF283596	374		398
AF283595	374		398
AF283594	374	• • • • • • • • • • • • • • • • • • • •	398
AF283593	374	• • • • • • • • • • • • • • • • • • • •	398
AF283592	374	• • • • • • • • • • • • • • • • • • • •	398
AF283591	374	• • • • • • • • • • • • • • • • • • • •	398
AF283590	374		398
AF283589	374	• • • • • • • • • • • • • • • • • • • •	398
AF283588	374	• • • • • • • • • • • • • • • • • • • •	398
AF283587	374	• • • • • • • • • • • • • • • • • • • •	398
AF283586	374		398
AF283585	374		398
AF283584	374	• • • • • • • • • • • • • • • • • • • •	398
AF283583	374	• • • • • • • • • • • • • • • • • • • •	398.
AF283582	374.	• • • • • • • • • • • • • • • • • • • •	398
AF283581	374	• • • • • • • • • • • • • • • • • • • •	398
AF283580	374	• • • • • • • • • • • • • • • • • • • •	398
<u>AF283579</u>	374	• • • • • • • • • • • • • • • • • • • •	398
AF283578	374	• • • • • • • • • • • • • • • • • • • •	398
AF283577	374	• • • • • • • • • • • • • • • • • • • •	398 398
AF283576	374		190 122
AF187030	398		323
AF310052	299	• • • • • • • • • • • • • • • • • • • •	323
AF310045	299	• • • • • • • • • • • • • • • • • • • •	326
AF171919	302 297	• • • • • • • • • • • • • • • • • • • •	121
<u>AF171897</u> AF290174	281		305
AF290173	281	• • • • • • • • • • • • • • • • • • • •	305
AF290171	281	• • • • • • • • • • • • • • • • • • • •	105
AF290170	281		105
AF290150	281	3	105
AF176252	398		22
AF176251	398		22
AF163907	398		122
AF163904	398	• • • • • • • • • • • • • • • • • • • •	22
<u>AF163901</u>	398	• • • • • • • • • • • • • • • • • • • •	22
AF163899	398	• • • • • • • • • • • • • • • • • • • •	22
AF163891	398		22
AF163890	398	• • • • • • • • • • • • • • • • • • • •	22
<u>AF288524</u>	401	• • • • • • • • • • • • • • • • • • • •	25
AF288523 AF288522	401		25
AF123530	303	3	27
AF123512	303	• • • • • • • • • • • • • • • • • • • •	27
AF206548	303		27
AF197867	401		25
V61197	303		27
NC 001945	15302		5326

NC_001821	14568	•••••	14592
AF141217	398	• • • • • • • • • • • • • • • • • • • •	422
AF201615	385	• • • • • • • • • • • • • • • • • • • •	409
AF077920	154		178
AF190632	398	• • • • • • • • • • • • • • • • • • • •	422
J01394	14911	• • • • • • • • • • • • • • • • • • • •	14935
AF193830	302	• • • • • • • • • • • • • • • • • • • •	326
U89181	401		425
U89171	401		425
AF217833	371		395
AF217822	374		398
AF217813	374		398
AF220408	413		437
AF126430	.398		422
AF090337	15123		15147 329
AF059111	305		
AF059053	305		329 327
AF099308	303		327
AF099295	303	• • • • • • • • • • • • • • • • • • • •	327
AF099294	303	••••••	327
AF099293	303	• • • • • • • • • • • • • • • • • • • •	422
AF160610	398		422
AF036280	398	••••••	422
AF036277	398		422
AF036274	398		326
AF194218	302		326
AF194216	302 14547		14571
NC_002009	14556		14580
NC 001941 NC 000877	15123		15147
NC 000846	14038		14062
U27551	401		425
AF089058	281		305
AF089055	281		305
AF089054	281		305
AF089046	281		305 296
AF089042	272		305
AF089039	281		305
AF089037	281		305
AF089026	281 281		305
AF089025 AF089024	281		305
AF089023	281		305
AF089021	281		305
AF089020	281		305
AF089016	281		305
AF089013	281		305 305
AF089012	281		305
AF089008	281		281
AF089006	257		305
AF089005	281 398		422
AF108696 AF108685	392		416
AF108677	398		422
AF145531	169		193
AF145511	169		193
U89627	360		384 384
U89623	360		327
AF181470	303 398		422
AF084075 U90303	398		422
U9030Z	398		422
U90301	398		422
U90300.	398		422
AF038883	392		416 416
AF019268	392		416
AF919357	192 56		80
512215 AF158628	39 6		422
AF138623	396		422
AF969191	401		425

AF091629	398		422
AF022063	398		422
AF022062	398		422
AF022060	398		422
AF022057	398	********	422
AF113500	384		408
AF113499	363		387
U69845	374		398 398
<u>U69810</u>	374		398
<u> U69808</u>	374		398
<u>U69799</u>	374		398
<u>U69796</u>	374		398
<u> U69795</u>	374		398
<u>U69794</u>	374		398
<u>U69793</u>	374 374		398
<u>U69792</u>	374		398
<u> </u>	374		398
<u>U69786</u>	374		398
<u>U69784</u>	374		398
<u>U69779</u> U69777	374		398
U69776	374		398
U69774	374		398
U69772	374		398
U69771	374		398
U69770	374		398
U69769	374		398
U69752	74		98
U69746	374		398 398
U69740	374		422
AF139057	398		15223
AF090339	15199		499
AF006275	475		499
AF006267	475		422
AF034969	398 398		422
AF028822 AF028821	398		422
AF061340	14547		14571
AF076093	401		425
AF076091	401		425
AF076072	401		425
AF076063	401		425 425
AF076059	401		425
AF076056	401		425
AF076053	401		425
AF076050	401 401		425
AF076049 AF076048	401		425
AF076045	401		425
U83314	401		425
V83318	401		425 327
<u> </u>	303		327
<u>U37302</u>	303		327
<u>U37296</u>	303 303		327
<u>U37289</u> U37286	303		327,
U37104	303		327
U37087	303		327
U87525	380		404
U87524	385		409 378
<u>U87523</u>	354		403
<u>U87522</u>	379 398		422
<u> </u>	329		353
U17862	328		422
U17860	328		422
U17859	329		353
U65274	396		422
U65267	398		422
<u>465260</u>	396 396		422
Ne2707	,,,		

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AF034738	398	422
AF034737	398	
AF034736	398	422
AF034735	398 398	422
AF034730	398	422
AF034729 AF034728	398	422
AF034727	398	
AF034724	398	
AF057132	396	422
U94805	401	
U94804	401	425
<u>U94803</u>	401	327
AF006251	303 303	
AF006249 AF006238	303	327
AF006234	303	327
AF006226	303	
AF006215	303	327
AF006214	303	327
AF006213	303 303	327
AF006212 AJ293419	398	
AJ293419 AJ293416	398	422
AJ293415	398	422
AJ293414	398	
AJ293412	398	422
AJ293418	398	422
<u>U07578</u>	398 302	326
<u>AJ004180</u> Y15695	432	456
Y15697	432	456
Y15696	432	456
AF015035	448	
AF015761	303	327
AF015758 AF015756	303 303 -	327
AF015754	303	327
U76052	401	425
AJ236834	398	422
<u>U83158</u>	302	326
<u>U83157</u>	304 302	326
<u>U83156</u> U83155	302	327
U83154	300	324
U81356	320	344
AJ277676	299	
AJ277675 AJ277672	299 299	323
AJ277671	299	323
Y11832	14568	14592
AJ388457	305	329
AJ388468	305 305	329
<u>AJ388459</u> U46167	398	422
AJ245673	400	424
AJ245638	400	424
AJ245678	400 400	424
AJ245677 AJ245676	400	424
AJ245675	400	424
AJ245674	400	424
Y16884	14038	14062
<u>U60769</u> U48955	40I	475
U48954	401	
U48944	401	425
V49941	401 401	4.3
U46942 U46941	401	425
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U48947	401	425	
U48946	401	425	
<u>U48948</u>	401	327	
<u> </u>	303	422	
<u>U66508</u>	398	422	
U66507	398 398	422	
<u>U66506</u> U66505	398	422	
U66504	398	422	
U66503	398		
U66502	398		
U66501	398	422	
U66500	398	422	
<u>U66499</u>	398	422	
<u>U66498</u>	398 302	326	
U63061 U63060	302	326	
U63059	302	326	
U63058	302		
U58386	398	422	
L11905	398		
U34672	398	422	
U34671	398	422	
Y14951	398 398	422	
<u>Y14371</u> L11909	398	422	
L11901	398	422	
L11904	398	422	
X94928	398	422	
U46770	302	326	
<u>U46769</u>	302	422	
<u>U46183</u> Y10728	398 299	323	
X95768	303	327	
X95767	303	327	
X86763	299	323	
X86754	299	323	
X86743	299 398	422	
AB035242 X60946	302	326	
AJ000029	398	422	
X82302	398	422	
X56291	398	422	
X56284	398	422	
AJ000022 X72005	398 398	422	
Y08814	398	422	
X60942	302	326	
X56290	398	422	
AJ000021	398 398	422	
AJ000024 V00654	14911	1493	5
X56286	398	424	
L19718	398	422	
U27543	401	425 367	
AB030025 U18258	343 169	193	
U18257	169	191	
U18253	169	193	
<u> </u>	169	193	
U17904	169 398	422	
D84202 D82889	398	422	
D32195	243	267	
D12191	398	422	
AB021098	398 398		
AB021097 AB021095	398		
AB021094	196		
AB021092	198	422	
88021091	196	***************************************	

AB001612	398		422
D84205	398		422
D84203	398		422
D34636	398		422
D34635	398		422
D12198	243		267
D33136	243		267
D32192	398		422
AB021099	398		422
AB021096	398		422
AB021093	398		422
AB021090	398		422
AB008539	15302		15326
008900BA	398		422
L12763	260 ·		284
L08032	401		425
L28941	398		422
L28937	398		422
AJ010056	269		293
AJ010054	269		293 293
AJ010053	269 ·		293
AJ010052	269		293
AJ010051	269	• • • • • • • • • • • • • • • • • • • •	293
AJ010050	269	•••••	293
AJ010049	269	•••••	293
AJ010048	269		293
AJ010047	269		431
<u> X95777</u>	407		293
AJ009879	269 269		293
AJ010055	303		327
<u>U08946</u>	303		327
<u>U08945</u> <u>U08944</u>	303		327
U08941	303		327
U08940	303	• • • • • • • • • • • • • • • • • • • •	327
X95775	303		327 327
X95774	303		327
X95764	303		310
AF040383	287		422
AF232023	400		422
AF232022	400 400		422
AF232021	322	*******	344
AF157466 AF157465	324		346
AF157464	324		346
AF157463	324		346
AF157460	321		343
AF231664	400		422 422
AF231663	400		422
AF231662	400		422
AF231660	400		422
AF231659 AF231658	400	***************	422
AF231657	400		422
AF231656	400		422
AF231644	400		422
AF231639			422
AF232019	400		422
AF232017	400		422
AF232014 AF318564	400 345		367
AF318563	345		367
AF318362	344		366
AF318561	344		366 366
AF318560	344		36.8 36.8
AF118552	344	******************	366
AFILESSE	344		403
AF118557 AF118555	361		403
AFILESSS	301		403
OFILESS1	361	• • • • • • • • • • • • • • • • • • • •	403

WC) 02/077278	
AFILR551	381	
AF318552	361	
AF318551	381	
AF318550	381	
AF318549	381 403	
AF318548	381	
AF238041	400	
AF326272	400	
AF326271	400	
AF326270	400	
AF326266	400 422	
AJ004340	302	
AJ004264	302n	
	•	
Databas	e: nt	
Poste	d date: Mar 2, 2001 12:20 AM	
Number	of letters in database: 2,863,827,88	5
Number	of sequences in database: 807,597	
Lambda	K	
1.37	0,711 1.31	
Gapped		
Lambda	K H 0.711 1.31	
1.37	0.711 1.31	
sensone bi	lastn matrix:1 -3	
Matrix: D.	ties: Existence: 5, Extension: 2	
Gab Lengt	Hits to DB: 39355	
Number of	Sequences: 807597	
Number of	extensions: 39355	
Number of	successful extensions: 15066	
Number of	sequences better than 10.0: 5706	
_	-	

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 39355
Number of Sequences: 807597
Number of extensions: 39355
Number of successful extensions: 15066
Number of sequences better than 10.0: 5706
length of query: 25
length of database: 2,863,827,885
effective HSP length: 17
effective length of query: 8
effective length of database: 2,850,098,736
effective search space: 22800789888
effective search space used: 22800789888
T: 0
A: 30
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)

WO 02/077278 98 PCT/IN01/00055

Table 11. BLAST analysis of primers 'mcb869' in nr database of NCBI. It demonstrates that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593033-24247-14777

Query-

(26 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the <u>BLAST FAQs</u>

Taxonomy reports

Distribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments	!
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(bits) Value

Score

Sequences producing significant alignments:

<u>52</u> 6e-06 qb[AF189111.1[AF189111 Cryptotermes austrinus cytochrome b ... <u>52</u> 6e-06 52 6e-06 qb|U86834.1|U86834 Phyllotis wolffsohni MSB 67270 cytochrom... gb[AF123633.1]AF123633 Perissocephalus tricolor cytochrome ... gb[AF123617.1|AF123617 Pipreola arcuata cytochrome b gene, ... gb|AF127202.1|AF127202 Hylopezus fulviventria cytochrome b ... gb/AF127194.1/AF127194 Grallaria guatimalensis cytochrome b... gb|AF217828.1|AF217828 Aspidelaps scutatus cytochrome b gen... qb/AF160578.1/AF160578 Hypogeomys antimena Hant555 cytochro... gb|AF009931.2|AF009931 Archocentrus centrarchus cytochrome ...
gb|AF091629.1|AF091629 Antilocapra americana cytochrome b (... gb[AF034967.1] Sigmoceros lichtensteinii cytochrome b gene,... gb|AF038290.1|AF038290 Antechinus sp. cytochrome b gene, mi... gb | U07577.1 | AMU07577 Antechinus melanurus mitochondrion cyt...
gb | U81343.1 | CFU81343 Chelus fimbriata cytochrome b gene, mi... emb|AJ222681.1|ABCYTOB Alcelaphus buselaphus mitochondrial ... gb | M99464.1 | PNZMTCYTB Planigale sp. cytochrome b gene, comp... emb|AJ225116.1|DNJ225116 Dryomys nitedula mitochondrial gen... gb | U25738.1 | PRU25738 Paradisaea raggiana cytochrome b gene,... 52 6e-06 52 6e-06 52 6e-06 52 6e-06 52 6e-06 gb U25736.1| PRU25736 Paradisaea rubra cytochrome b gene, mi... gb|U15202.1|SMU15202 Seleucidis melanoleuca mitochondrion c... gb|U15204.1|PR15204 Paradisaea raggiana mitochondrion cytoc... emb|X56290.1|MIDDCYTB D.dama mitochondrion cyth gene for cy...
emb|X56286.1|MIAACYTBA A.americana mitochondrion cyth gene ... 52 6e-06 52 6e-06 46 3e-04 dbi|D88639.1|D88639 Anoa depressicomis mitochondrial DNA f... dbj|D82890.1|D82890 Bubalus depressicornis mitochondrial DN... gb AF119261.1 AF119261 Peromyscus maniculatus cytochrome b ... 45 3e-04 gb/AF123615.1/AF123615 Rupicola rupicola cytochrome b gene,... 45 3e-04 45 3e-04 gb AF160603.1 AF160603 Apodemus sylvaticus Asyl588 cytochro... gb|U62697.1|CCOLCYTB2 Charadrius collaris cytochrome b (cyt... 45 3e-04 gb|U62685.1|CBICCYTB2 Charadrius bicinctus cytochrome b (cy... gb AF022071.1 Madoqua guentheri cytochrome b (cytb) gene, ...
gb AF022070.1 Madoqua kirkii cytochrome b (cytb) gene, mit... 45 3e-04 45 3e-04 45 3e-04 gb | U37293.1 | CCU37292 | Cepphus columba cytochrome b gene, mitoc...
gb | U37292.1 | CCU37292 | Cepphus carbo cytochrome b gene, mitoc...
gb | U37292.1 | CCU37292 | Cepphus carbo cytochrome b gene, mitoc...
gb | U37292.1 | CCU37292 | Brachyramphus marmoratus perdix cytoch... 45 3e-04 45 3e-04 45 3e-04 45 3e-04 45 3e-04 gb[AF082055.1|AF082055 Rupicola rupicola cytochrome b gene,... gb|U72770.1|JMU72770 Jabiru mycteria cytochrome b gene, mit... 45 Je-04 45 Je-04 gb/U07578.1/OCU07578 Dasycercus cristicauda mitochondrion c... Sb[AF0]1908.1|GOCCCYTB] Geopsittacus occidentalis cytochrom... 45 3e-04 45 3e-04 46 3e-04 emb|AJ004231.1|SBAJ4231 Sula bassana mitochondrial cyth gen...
emb|AJ004230.1|SBAJ4230 Sula bassana mitochondrial cyth gen... emb[AJ004229.1]SBAJ4229 Sula bassana mitochondrial cyth gen... emb|AJ004232.1|SBAJ4232 Sula bassana mitochondrial cyth gen... 45 Je-04 45 36-04 gb[U88865.1] Pomacentrus sp. cytochrome b (cytb) gene, mito... 45]e-04]e-04 gb[U90001.1]MBU90001 Morus bassanus cytochrome b gene, mito...
gb[U63057.1]SMU63057 Brachyramphus marmoratus perdix cytoch... 45 dbi|AB036404.1|AB036404 Rana porosa brevipoda micochondrial... dbj|AB0]6402.1|AB0]6402 Rana porosa brevipoda mitochondrial...
dbj|AB0]6400.1|AB0]6400 Rana porosa brevipoda mitochondrial... 3--04 34-04 3--04 dbj[AB0]6]98.1[AB0]6]98 Rana porosa porosa mitochondrial CN... 45 3=-04 qb|U19611.1|JMU19611 Jabiru mycteria cytochrome b gene, mit...
emb|X92519.1|HACYTB H.ampullatus cytochrome b gene (complet... 3=-04 45 3=-04 GB|[090]4, ||GAEMTC/TBA| Galeocerdo cuvier mitochondrial cyto...
GB|[090]], ||CPLMTC/TBB| Carcharhinus porosus mitochondrial c... 3=-04 0.001 qb[AY015012.1] Crypturellus tacaupa micochondrion, parcial ... 4.4 0.001 qb[AF074591.1]AF074591 Petrochelidon pyrrhonota cytochrome ... 44 0.001 qb[AY005212.1] Poospiza whicil isolate 2 cytochrome b (cytb... gb[AY005211.1] Poospira whitil isolate 1 cytochrome b (cytb... a.aal qb|AF187122.1|AF187122 Cryptotermes tropicalis cytochrome b...
qb|AF187120.1|AF187120 Cryptotermes secundus cytochrome b |... 0.001 0.001 qb[AF187119.1[AF187118 Cryptotermes primus isolate 2 cytoch ... 300.0 Cryptotermes primus isolate i cytoch ... 901AF193117.11AF193117 901AF193115.11AF193115 Cryptotermes dudlyl cytochrome b (Cy... 0.001 44 0.991 qbiAF112149 LIAF112149 Ovie canadensis cytochrome b gene. p ... 0.001 Ovie canadensis canadensis cytochrom... GDIAFILILIZATION Ovie canadenate neteont cytochrome b . 0.901 golafillig LLAFILLIS 44 0.001 901AF991779.11AF991779

		44	0.001
gb AF081989.1 AF081989	Vireo cassinii cassinii specimen-vou		0.001
gb AF081988.1 AF081988	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081987.1 AF081987	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081986.1 AF081986	Vireo cassinii cassinii specimen-vou	44	
qb AF081985.1 AF081985	Vireo cassinii cassinii specimen-vou	44	0.001
95 AF081984.1 AF081984	Vireo cassinii cassinii specimen-vou	44	0.001
dp AF081984.1 AF081984	Vireo cassinii cassinii specimen-vou	44	0.001
gb[AF081983.1 AF081981	VICEO CASSIMII CASSIMII SPECIMEN VOUL	44	0.001
gb AF081982.1 AF081982	Vireo cassinii cassinii specimen-vou		0.001
gb AF081981.1 AF081981	Vireo cassinii cassinii specimen-vou	44	0.001
95 AF081980.1 AF081980	Vireo cassinii cassinii specimen-vou	44	
gb AF081979.1 AF081979	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081978.1 AF081978	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081977.1 AF081977	Vireo cassinii cassinii specimen-vou	44	0.001
db AF0819//.1 AF0819//	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081976.1 AF081976	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081975.1 AF081975	Alieo cassium cassium abecimen-Add	44	0.001
gb AF081974 . 1 AF081974	Vireo cassinii cassinii specimen-vou		0.001
gb AF081973.1 AF081973	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081972.1 AF081972	Vireo cassinii cassinii specimen-vou	44	
gb AF081971.1 AF081971	Vireo cassinii cassinii specimen-vou	44	0.001
gb AF081970.1 AF081970	Vireo solitarius alticola country US	44	0.001
gb AF081969 . 1 AF081969	Vireo solitarius alticola country US	44	0.001
GD AF061969.11RE001969	Vireo solitarius alticola country US	44	0.001
gb AF081968.1 AF081968	Vireo solitarius alticola country US	44	0.001
gb AF081967.1 AF081967	Vireo solitarius solitarius specimen	44	0.001
gb AF081966.1 AF081966	Vireo solitarius solitarius specimen	44	0.001
gb AF081965.1 AF081965	Vireo solitarius solitarius specimen	44	0.001
gb AF081964.1 AF081964	Vireo solitarius solitarius specimen		0.001
gb AF081962.1 AF081962	Vireo flavifrons specimen-voucher LS	44	0.001
gb AF081961.1 AF081961	Vireo flavifrons specimen-voucher LS	44	0.001
gb AF081950 .1 AF081960	Vireo leucophrys leucophrys specimen	44	
qb AF081959.1 AF081959	Vireolanius leucotis leucotis cytoch	44	0.001
gb AF112405.2 AF112405	Barbus ancolus cytochrome b (cytb) g	44	0.001
gb AF144317.1 AF144317	Amphiprion ocellaris isolate 3 haplo	44	0.001
gb AF144316.1 AF144316	Amphiprion ocellaris haplotype 3DH11	44	0.001
GD AF144316 . L AF144316	Amphiprion ocellaris haplotype 30H15	44	0.001
gb AF144315.1 AF144315	Amphiprion ocellaris isolate 2 haplo	44	0.001
95 AF144314.1 AF144314	Amphiprion ocellaris isolate 1 haplo	44	0.001
gb AF144313.1 AF144313	Amphiprion ocellaris haplotype 3DH12	44	0.001
gb AF144312.1 AF144312	Amphiprion ocellaris haplotype 3DH1	44	0.001
gb AF144311.1 AF144311	Amphiprion ocellaris isolate 2 haplo	44	0.001
gb AF144310.1 AF144310	Amphiprion ocellaris isolate 1 haplo	44	0.001
gb AF144309.1 AF144309	Amphiprion occilaris isolate i napio	44	0.001
ref NC 001567.1 Bos t	aurus mitochondrion, complete genome	44	0.001
gb AF212124.1 AF212124	Anolis schwartzi cytochrome b gene,	44	0.001
gb AF182706.1 AF182706	Phapitreron amethystina cytochrome b:	44	0.001
gb AF010406.1 AF010406	Ovis aries complete mitochondrial ge	44	0.001
gb AF096452.1 AF096452	Platysteira cyanea cytochrome b gene	44	0.001
gb AF283619.1 AF283619	Elaphe obsoleta LSUMZ39162 cytochrom		0.001
q5 AF283618.1 AF283618	Elaphe obsoleta LSUMZ H15896 cytochr	44	0.001
gb AFZ83608.1 AFZ83608	Elaphe obsoleta LSUMZ H14782 cytochr		0.001
95 AF283602 . 1 AF283602	Elaphe obsoleta LSUMZ H3388 cytochro	44	0.001
gb[AF310069.1]AF310069	Flaenia martinica cytochrome b gene	44	0.001
95 AF146616 . 1 AF146616	Actophilornis africanus cytochrome b	44	0.001
qb AF271410.1 AF271410	Galago moholi cycochrome b (cyc b) g	44	0.001
gb[AF290139.1]AF290139	Peucedramus taeniatus cytochrome b (9.001
reciNC 002504.11 Lama	paces mitochondrion, complete genome	44	a.aar
gb AF153901.1 AF163901	Microtus ochrogaster cytochrome b gs	44	0.001
qb[AF119263.1[AF11926]	Myopus schisticolor cytochrome b gen		0.001
gb AF119259.1 AF119259	Synapcomys borealis cytochrome b gen	44	0.001
gb AF288454.L AF288454	Nyctereutes procyonoides koreensis C	44	0.001
95 AF153895. LIAF163895	Microtus gragalia cytochrome B (cyt8	44	0.001
gb AF12]549.1 AF12]549	Machaeropterus regulus ecriolacus cy	4.1	0.001
qb AF12]547.1 AF12]647	Machaeropterus pyrocephalus cytochro	44	0.001
95 AF123545. 1 AF123545	Kenopipo atronitena cytochrome b gen	44	0.001
96 AF12 1645 . 1 AF12 1645	Pipra fascilcauda cytochrome b gene	44	0.001
96 AF123634 . 1 AF123634	Pyroderus scutatus cytochrome b gene	-11	0.00%
95 AF123532. 1 AF123532	Cephalopterus ornatus cytochrome b g	===	100.0
95 AF121529 . LAF121529	Turdampella cryptolophua cytochrome porphyrolaema porphyrolaema cytochro	_44	0.001
APISTEL TAPISTE	Ampelioides technolic cytochrome b ge	-11	0.001
95 AF121519.11AF121512	Pipeala chiacolapidata cytochroma b	4.1	0.001
PIRELIANIE LIAPIZISIE	Rupicala periviena cytochroma b gene	4.4	0.071
SPINELISIA LIAPUNISIA	Dollocate estatest sysochrome b gene	-	0.071
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95 AF127201.1 AF127201 Myrmoth	mera campanisona cytochrome b	44	0.001
chiag127192 1[AF127192 Gralla	cia ruficapilla cytochrome b g	44	0.001
chiagrazias 1 AF127189 Grallas	ria varia cycochrome b gene, p	44	0.001
-LINETATRAG TIAFIGTRAG Serico	mis frontalis cytochrome b ge	44	0.001
chiam197847 11AF197847 Pardale	otus striatus cytochrome b gen	44	0.001
flac nonsse 1 Hippopotamus	amphibius mitochondrion, comp	44	0.001
TOFING 002079 11 Carassius au	catus mitochondrion, complete	44	0.001
FINC 001794 11 Macropus robu	iscus mitachondrion, complete	44	0.001
glac consid 11 Didelphia vi	rginiana mitochondrion, comple	44	0.001
115701612 1 AF201612 Stomato	arhinus sp. CU79703 cyotchrome	- 4 4	0.001
gb AF097931.1 AF097931 Amphip	rion clarkii cytochrome b gene	44	0.001
gb AF097927.1 AF097927 Amphip	rion ocellaris cytochrome b ge	44	0.001
gb J01394.1 BOVMT Bos taurus	mitochondrion, complete genome	44	0.001
gb AF168760.1 AF168760 Apalone	spinifera isolate TXsc cytoc	44	0.001
	spinifera isolate TXki cytoc	44	0.001
	spinifera isolate TXcc cytoc	44	0.001
	spinifera isolate NMrg cytoc	44	0.001
	nelidon rufocollaris isolate E nelidon rufocollaris isolate E	44	0.001
	delicon funccitatis isolate a	44	0.001
	mexicanus cytochrome b (cytb) us lentiginosus cytochrome b g	44	0.001
	alba cytochrome b gene, partia	44	0.001
	nerodias cytochrome b gene, pa	44	0.001
	ja multifasciata cytochrome b	4.1	0.001
	nouthia cytochrome b gene, com	44	0.001
	ida colubrina cytochrome b gen	44	0.001
gb AF217834.1 AF217834 Laticate gb AF217831.1 AF217831 Callion	phis japonicus cytochrome b ge	44	0.001
11 17077 1 1 2 2 1 7 9 7 7 Michael	sides euroxanthus cytochrome D	44	0.001
: 1. 2017010 1125217919 Dyreda	lia coronata cytochrome b gene	44	0.001
- 1 1 35217015 Augtre	lang superbus cytochrome b gen	44	0.001
	ra humeralis specimen-voucher	44	0.001
- 14-500000 1 13-700078 Funca 2	erra isolate 62 cytochrome b g	44	0.001
gb AF209933.1 AF209933 Euura	atra isolate C cytochrome b ge	44	0.001
gb AF059104.1 AF059104 Marmaro	onetta angustirostris cytochro	44	0.001
	etta specularoides cytochrome	44	0.001
	ampus barbouri haplotype PH.22	44	0.001
gb AF192646.1 AF192646 Hippoca	impus barbouri haplotype PH.13	44	0.001
- 1 COC14 1 3 57 60614 Cricato	mys gambianus Cgam518 cytocht	44	0.001
· last cocta alast socia Criceto	mys emini Cemi531 cytochrome	44	0.001
:	amys emini Cemi530 cytochrome	44	0.001
gb AF160611.1 AF160611 Criceto	omys emini Cemi637 cytochrome	44	0.001
gb AF160610.1 AF160610 Criceto	mys emini Cemi636 cytochrome	44	0.001
gb AF160604.1 AF160604 Calomys	scus bailwardi Cbal576 cytochr s majori Emaj642 cytochrome b	44	0.001
	majori Emajo42 Cycochrome b	44	0.001
	majori Emaj639 cycochrome b	44	0.001
· Languages 1 AFTENSET Fliggers	majori Emaj638 cytochrome b	44	0.001
· Lagrange Tings Coses Eliumis	majori Emaj614 cytochrome b	44	100.0
LINESCOSEA ILASISOSSA ELIUTUS	majori Emaj617 cytochrome b	44	0.001
gb[AF160553.1[AF16055] Eliurus	majori EmajS73 cycochrome b	33	0.001
ablaF160552.1 AF160552 Eliurus	majori Emaj556 cycochrome b majori Emaj561 cycochrome b	44	0.001
	majori Emaj443 cytochrome b	44	0.00L
	majori Emaj444 cytochrome b	44	0.001
125026267 11A5036207 Damelia	cus nygargus cytochrome b (cy	44	0.001
- 1125076786 1125076786 Omer le	wener cytochrome b (cytb) ge	44	0.001
qb[AF036283.1[AF036281 Antilog	e cecyicapra cytochrome b (cy	44	a.aal
qb AF036281.1 AF036281 Ancidos	cas marsupialis cycochrome b	4.3	0.00L
	phus oryx cytochrome b (cytb) phus euryceros cytochrome b (4.4	0.001
-LIACO36274 11 Terracerus miad	iricornia cytochrome b (cytb)	4.4	0.001
- alve colosi ii Onia acian mi	Forhondrion, complete genome	44	0.00L
abjafionegn 1 AFLORESH MICTORY	ADMAN WINGERS CACOCUEOMG & IC	44	0.001
gb AF108682,1 AF108682 Rhipido	mys nicela cycochrome 8 (cycs	44	9.901
95 AF10867] LIAF10967] Thomaso	mys dipline cytocheome B (cytB	3.3	9.991
1 1 A TO 4 2 7 7 0 1 1 A F 0 4 2 7 7 0 Magamus	telacue vuguandenale cycochrom	- 4.3	9.091
wings and the Munclesus munti	ak cytochrome b gene, mitocho	_11	0.051
-laggerger (laggerent) Grenell	a coerticoalda cytochtoma o q	-4.3	0.001
Scenell IEBERTAIDE	a coerstenatha cytochemma b g .	71	

gb AF084074.1 AF084074 Lagenorhy	mchus albirostris cytochrom	44	0.001
gb AF090750.1 AF090750 Gobio got	Dio balcanicus cytochrome b	44	0.001
	ilus columbianus columbianus	44	0.001
	ilia columnianda columnama	44	0.001
gb AF157917.1 AF157917 Spermophi	ilus washingtoni isolate 589	44	0.001
gb AF157936.1 AF157936 Spermophi	ilus washingtoni isolate S88		0.001
gb AF157915.1 AF157915 Spermophi	ilus richardsoni isolate S63	44	a.aal
chia=157914 1[AF157914 Spermoph	ilus richardsoni isolate S62	44	
ablasistate 1 AF157912 Spermonh	itus undulatus isolate 560 C	44	0.001
gb AF157906.1 AF157906 Spermophi	ilus undulatus isolate SSS c	44	0.001
	ilus elegans elegans isolate	44	0.001
	llus columbianus columbianus	44	0.001
	ilus columbiants columbiants	44	0.001
	ilus citellus isolate S118 c		0.001
-hise167858 11AF157858 Spermophi	ilus citellus isolate S117 c	44	
135157939 1 35157839 Spermophi	ilus elegans elegans isolate	44	0.001
-blacoggagg 1 AF030497 Crocidura	hrunnea cytochrome b (cyt	44	0.001
qb U03541.2 LAU03541 Lenoxus api	icalis cytochrome b gene, pa	44	0.001
	pendiculatus cytochrome b (c	44	0.001
	la tuba cytochrome b (cytb)	44	0.001
	is the experience of the first	44	0.001
	rus sajica cytochrome b (cy	44	0.001
	whiteheadi cytochrome b ge		0.001
-hlas094621 11A5094621 Eminia 16	epida cytochrome b gene, par	44	0.001
Laggaria 1 Aggaria Hymergeri	is atriceps cytochrome b gen	44	
INSIECIAR ILASIEGIAR Phascolar	ctos cinereus cytochrome b	44	0.001
-LISTISSEST TIARTSSEST GEOMYS DE	irgarius ozarkensis cytochro	44	0.001
gb AF158694.1 AF158694 Geomys bu	irsarius majusculus cycochro	44	0.001
	rearius bursarius cytochrom	44	0.001
	rsarius missouriensis cytoc	44	0.001
	ilus citellus cytochrome b (44	0.001
	depressicomis cytochrome b	44	0.001
	legressicornia cycocmome b ce	44	0.001
	es gliroides cytochrome b ge	44	0.001
	ursinus cytochrome b gene,	44	0.001
gb AF022065.1 Tragelaphus eury	eros cytochrome b (cytb) ge		0.001
The manage of the tobus allinging	mus cytochrome b (cytb) gen	44	0.001
This manages 1! Barilone certical	ora cytochrome b (cytb) gene	44	0.001
In reconst 1 Tracelating of VX	cytochrome b (cytb) gene, m	44	0.001
-blacksons ti Antidoress margus	pialis cytochrome D (Cyto) 9	44	0.001
	sees amon checkings a (chem	44	0.001
Lucases 1 pettegges Purhon seha	e cytochrome b (cytb) gene,	44	0.001
-Litteggaa ilittigggaa Lichanura t	rivirgata cytochrome b (cyt	44	
-Llas143193 1[AS143193 Enimenhe]	lus sp. cytochrome b (cytb)	44	0.001
13 -1 21 222 1 1 3 F1 21 222 Amphingic	n ocellaris isolate 8 cytoc	<u> 4÷</u>	0.001
12 =000025 1 1 2 =096625 Kohus el 1	lingiprymnus defassa cytochr	-44	0.001
tingoccia tingoccia Kohug ell	lingiprymnus ellipsiprymus C	44	0.001
95 AF081052.1 AF081052 Eulemur	ubrivencer cycochrome b (cy	44	0.001
Lamparona Tiamonida Fulenut M	macaco macaco cytochrome b (44	0.001
12 TOO TOAR TIAFORTOAR FULLEMIT	fulyus albifrons cytochrome	44	0.001
"La magazaca di Amagazaca Fiminia	ongicauda cytochrome b gene	44	0.001
- 1 - 7010057 1 W33 770957 Winnone	ramus amphibius complete mi	44	0.001
Langeon 1 CT 175506 Chiamidera	lauterbachii cytochrome b g	· 44	0.001
Lungeon 1 CC176504 Chlamydera	cerviniventria cytochrome b	44	0.001
-LITTEENS TIASTITESOS Ambigornia	subalaris cytochrome b gene	44	0.001
- Luncear Maggreson Aschboldia	naquensis cycochrome b gene	44	0.001
LUTSEOR TIATUTESOR Ambivornia	inornatus cytochrome b gene	44	100.0
14 5024969 1145034969 Connochae	tes taurinus cytochrome b g	44	0.001
112061876 112F051876 Phodeug C	cellatus cytochrome b (cytb	44	0.001
-blaseggoog llaseggoog Viceo plu	mbeus plumbeus specimen-vou	44	0.001
This service tiarnazone Vireo plu	mbeus plumbeus specimen-vou	44	0.001
-blaspazons llaggaggs Vices plu	mbeus plumbeus specimen-vou	44	0.001
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AFRICATION LIAFORTON Vices plu	imbeus plumbeus specimen-vou	44	0.001
Incompany Liacontono Vices plu	umbeus plumbeus specimen-vou	44	0.001
95 AF091999.1 AF081977 Viceo plu	imbeua plumbeua apecimen-vou	-4:4	0.001
951AF081999 11AF081229 Viceo plu	imbeus plumbeus specimen-vou	44	0.001
ablaF981377.11AF991397 Virao plu	imbeus plumbeus specimen-vou	-4-4	a.aat
ablaf041795 LIAF041795 VLC40 PLU	mbeus plumbaus specimen-vou	_4 1	0.001
ablafos1225.11AF991925 Vicao plu	mbeue plumbeue epecimen-vou	4.3	0.001
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qb AF081991.1 AF081991 Vireo plumbeus plumbeus specimen-vou	44	0.001
qb S73150.1 S73150 cytochrome b (Spermophilus richardsonii=	44	0.001
gb S73150.1 S73150 cytochrome b [Spermophilus richardsonii=	44	0.001
qb AF012235.1 AF012235 Cryptomys hottentotus natalensis Cyt	44	0.001
gb U53580.1 NCU53580 Nycticebus coucang cytochrome b (cyt b	44	0.001
gb US3577.1 EFUS3577 Eulemur fulvus rufus cytochrome b (cyt	44	0.001
qb/U53576.1 EFU53576 Eulemur fulvus collaris cytochrome b (44	0.001
gb/U95512.1/ESERCYTB2 Eptesicus serotinus 3' cytochrome b (44	g.ggi
gb/U95508.1 PKUHLCYTB2 Pipistrellus kuhli 5' cytochrome b (44	0.001
gb/U17868.1/BTU17868 Budorcas taxicolor taxicolor cycochrom	44	0.001
gb/U17867.1 BTU17867 Budorcas taxicolor bedfordi cytochrome		0.001
gb/U17860 1/ODU17860 Ovis dalli cytochrome b gene, mitochon	44	0.001
abiu17859 1 OCU17859 Ovis canadensis cytochrome b gene, mit.	44	0.001
THIS TOLDESS 1 LASPOIDESS ACOMVS SPINOSISSIMUS MITOCHONGELAL	44	0.001
- Larga 4736 1 AFG34736 Capra falconeri cytochrome D (cyto)	44	0.001
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blacarana Il Ovia dalli dalli cytochrome b (cytb) gene, m	44	0.001
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birmaga 1 MMT172038 Monodon monoceros cytochrome b (cytb),	44	0.001
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historia il Mirrorrovra Mureria longicaudata cytochrome b gen	44	0.001
This age is suppression sheep mitochondrial cycochrome b (Cy	44	0.001
the page 47 1 a road 47 Coccurs americanus cytochrome b gen	44	0.001
ilamanage ilamanage Annechinus minimus cytochrome b gene	44	0.001
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thencenes stategons and undulate cytochrome b gene, par	44	0.001
gh AF059092.1 AF059092 Anas superciliosa rogersi cytochiche	44	0.001
gb/AF059091.1/AF059091 Anas sparsa cytochrome b gene, parti	44	0.001
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gb AF059078.1[AF059078 Anas laysanensis cycochrome b gene,	44	0.001
gb AF052240.1 AF052240 Anairetes flavirostris cytochrome 5	44	0.001
gb AF006240.1 AF006240 Microspingus cassinii cytocarome b	44	0.001
gb AF006227.1 AF006227 Dacnis cayana cytochrome b (cytb) ge gb AF047447.1 AF047447 Oryx leucoryx cytochrome b gene, mic	44	0.001
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blacogize 1 a F078178 Paeudalonex sechurae cytochrome b (C	44	0.001
the margine illamonation wilnes renda cycochrome b (cytb) gen	44	0.001
Liveast ilasumtsovia Antechinus stuartii cytochrome b gen	44	0.001
ilicato ilacingoro Angechinus swainsonii cytochrome b Se	44	0.001
Ligares liaminates agrections haso cytochrome b gene, mit	44	0.001
gb U87138.1 TVU87138 Trichosurus vulpecula cytochrome b (Cy	44	0.001
gb U07590.11 PMU07590 Planigale maculata mitochonderon cytoc	44	0.001
emb AJ004326.1 PTAJ4326 Phylloscopus trochilus mitochondria	44	0.001
gb AF020255.1 AF020255 Cyclura nubila cytochrome b (cytb) g emb Y19184.1 LPA19184 Lama pacos complete mitochondrial genome	44	0.001
	44	0.001
gb U88862.1 Amphilophus citrinellum cytochrome b (cytb) ge gb U88859.1 Thorichthys aureum cytochrome b (cytb) gene, m	44	0.001
Lingues 11 Thorishebus of aureum cycochrome b (Cycb) gen	44	0.001
Linguist 11 Wasiahahan lahaidang cytochrome D (CYto) gent	44	0.001
blerance il Warichehum carnichia cycochrome D (cyco) gene,	44	0.001
Livings, ilminocen micronia robustus complete mitochondii	44	0.001
Liveries il cormiscs challed a gementing cytochrome b gene	44	0.001
ablusiss 1/CLUSISS Chelodina longicollis cytochrome b gen	44	0.001
db U75354.1 LUU75354 Leptomyrmex unicolor cytochrome b gene db U77332.1 CCU77332 Cymnorhinus cyanocephala cytochrome-b	44	0.001
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Listance I lateving godelanhis trapopala mitochondria	44	100.0
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blazzares ilongrous and damah mitochondrial cytochrome	-4-4	0.001
gb[M79466.1]PMLMTCTTB Perameles nasuca cycochrome b gene. c	44	0.001
ab[m37452.1] THOMTCYTB Thylacinus cyncocephalus cytochrome b	44	0.001
abim39460 lipavmTCYTB Desyurus hallucatus cytochrome b gane		0.001
ablu25717 1 PMU25717 Paradisaes minor cycochrome b gene, mi	4!	0.001
Livising (Faittein Friedling Albertiel mitochondrion Cyto	4.4	9.001
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emb AJ004792.1 HCAJ4792 Hippolais caligata ssp. rama mitoch	44	0.001
qb/U15718.1/RSU15718 Ramphocelus sanguinolentus cytochrome	44	0.001
gb/L11905.1/CGYMTCYTBD Cratogeomys g/mnurus mitochondrial c	44	0.001
qb U34679.1 POU34679 Philander opossum cytochrome b light s qb L11907.1 CGYMTCYT35 Cratogeomys goldmani rubellus mitoch	44	0.001
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transatiletown & longinostris cytechrome b gene (compl	44	0.001
Time carry alactrostria anchus campestris cytochicme b gene, m	44	0.001
" : language a language a anguilla interioris mitochondrial C	44	0.001
dbj[A3006953.1[A3006953] Carassius auratus langsdoffi mitsch	44	0.001
emb Z73492.1 MTPTRCYTS P.trochilus mitochondrial cytochrome	44	0.001
dbj[AB035239.1]AB035239 Osteoglossum ferreirai mitochondria	44	0.001
emb X92532.1 MMCYTB2 M.monoceros cytochrome b gene (complet emb X74260.1 MIVOCYT3 V.olivaceus mitochondrion gene for Cy	44	0.001
	44	g.ggl
S. Longinostris mitochondrion cyth Ge	44	0.001
Three limitations B violectus mitachondrian gene for Cy	44	0.001
bignida micochondrial cytochrome b	44	0.001
emb X82302.1 MIPFCYTEG P. fasciata mitochondrial cytochrome	44	0.001
emb x56284.1 MIOACYT3 O.aries mitochondrion cyts gene 101	44	0.001
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ilenance ilenticement ludovicianus mitochondrion gene for	44	0.001
I language a lighter cyroc w liberiensis mitochondrial cytochro	44	0.001
iteracia ilutua cure u amphibius mitechondrial cytochrome	44	0.001
emb X56287.1 MIGCCYT3 G.camelopardalis mitochondrion cyth g	44	0.001
emb X74253.1 MIEFCYTB E.fastuosus mitochondrion gene for Cy emb X60941.1 MIEACB33 Epimachus albertisii mitochondrial ge	44	0.001
The same il MIDMCOTT D. macmificial mitochondrion gene for C	44	0.001
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i transcri i latarry des parints complete mitochondrial genome	_ 4 4	0.001
blycopic ilutawcer: a macgregoriae mitochondrial gene iot	44	0.001
emb X92530.1 LACYTB L.albirostris cytochrome b gene (comple	44	0.001
gb U09265.1 CAU09265 Coccyzus americanus mitochondrion cyto dbj A8023906.1 A8023906 Petaurista leucogenys mitochondrial	44	0.001
willings one liangs on persuriara leucogenys mitochondrial	44	0.001 0.001
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	44	0.001
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dbj [D88627.1 D88627 Bubalus bubalis mitochondrial DNA for c	44	0.001
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db11082989 11092889 Boe javanteus mitochondelal DNA for cyc	44	0.001
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" . Language Lianguage Comma higging mitochondrial DNA for	4.1	0.001
" . Language Lianguage Comma higging mitochondetal DNA Cor	4.1	0.001
db1 ABQQ4Q71,1 ABQQ4971 Capra hiccus micochondctal DNA Coc	11	0.001
dbilasonass ilasonass Capra aggarda micochondrial DNA C.	, 4.4	9.091
db11099540 i1099540 Anos depressioneris micochondrist una t db11099517 i1099517 Subside bubside micochondrist DNA (or c	_• •	9 996

to the second se	44	0.001
db1 D88634.1 D88634 Bubalus bubalis micochondrial DNA for C	44	0.001
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" Location tipopera publica hubalia micochondriat DNA Lut L	44	0.001
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illiance allegaet Bubalus mistlesi mitochondrial DNA tor	44	
The state of the s	44	0.001
Bog javanicus mitochondrial gene tor	44	0.001
Tales altaics mitochendrial cyto ge	44	0.001
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gb U07565.1 HAU07565 Hippopotamus ampnibius micochondia	44	0.001
ab u10367.1 PVU10367 Ptilonorhynchus Violaceus mrtdenonur	44	0.001
gb/U10364_1 CMU10364 Chlamydera macuiata mitotandition	44	0.001
emb Z96068.1 ASZ96068 Acomys spinosissimus bux tot mits	42	0.005
gh U76507.1 AIU76507 Amblyornis inormatus eyebeniche b gene	40	0.021
chlaf157466.1[AF157466 Lepus timidus eytochrome b (Cyb)	40	0.021
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gbiAF182711.1 AF182711 Geopelia cuneaca Cycochiome b game	40	0.021
gb AF182687. 1 AF182687 Columbina picur cycochrome by	40	0.021
gblaf155422.1[AF155422 Sigmodon denrognating Cyclemonic	40	0.021
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gblaf155589, 11AF155599 Sigmodon ochrognathus leolate Boenda	47	9.021
db AF12351 1 1 AF123511 Teachyphonus darmaudt of	42	g.gzt
ab AF754947 1 AF754947 Ureus april 444 Cycochtoms	12	9.921
gbiAF295511.11AF295511 Podercie electe eyectione of FK. 14	17	0.011
CERING 000994 II Cavia porcellus complete mitochondelal genome	_12	3.011
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gb AF004572.1 AF004572 Arvicanthis niloticus cytochrome b (40	0.021
gb/AF088932.1/AF088932 Sminthopsis psammophila cytochrome b	40	0.021
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gb U62697.1 ORUCYTB2 Oreopholus ruficollis cytochrome b (cy	40	0.021
GDIU67881.11CACITEZ CHALACETTA AGRICALTA CITATION - 1-1	7.8	0.084
aninesini diaratina diaratina deregga elegatina	-30	0.084
emb/AJ004315.1/HCAJ4315 Hippolais caligata mitochondrial cy	79	0.004

Alignments

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<u>U15202</u> U15204	872		847
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U62685	179	• • • • • • • • • • • • • • • • • • • •	157
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AF022070	866	*****	844
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<u>U37293</u>	774	• • • • • • • • • • • • • • • • • • • •	752 752
<u>U37292</u>	774		752
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<u>572770</u>	869 ·		847
<u>U07578</u> AF031908	187		165
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AJ004229	773	• • • • • • • • • • • • • • • • • • • •	751
AJ004232	773	••••••	751
U88865	850	* * * * * * * * * * * * * * * * * * * *	828 514
<u>1000en</u>	536		514 751
<u>U63057</u>	773 173	• • • • • • • • • • • • • • • • • • • •	151
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AB036398	173		151
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AF144312	161	gg	136 136
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U81336	791 452		427
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H22432	967		444

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X82302	869		844
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Y08813	869	gg	
X56287	869	gg	844
X74253	872	gg	• •
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088633	869		844
D88632			•
D88610 ·	869		844
088628	869	• • • • • • • • • • • • • • • • • • • •	844
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284202	869		644
092991	169		544
D92922	169	· · · · · · · · · · · · · · · · · · ·	144
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012121		******************************	

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AB004072	869	gg.	844
AB004071	869	gg.	844
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D88637	869	· · · · · · · · · · · · ·	844 844
D88634	869	aa	844
D88631	869	aa	844
D88629	869		844
D84205	869 869		844
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X92531 U07565	869		844
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U10364	773	gg.	748
Z96068	869	g	844
U76507	773	·····	749 772
AF157466	791		774
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AF155499 AF155385	669		650
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9617775	447		

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AF088932	869		850
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•			

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,863,827,885 Number of sequences in database: 807,597

Lambda K H 1.37 0.711 1.31

Gapped

Lambda K H

S1: 12 (24.3 bits) S2: 16 (32.2 bits)

1.37 0.711 1.31

Matrix: blastn matrix:1 -3 Gap Penalties: Existence: S, Extension: 2 Number of Hits to DB: 19068 Number of Sequences: 807597 Number of extensions: 19068 Number of successful extensions: 7580 Number of sequences better than 10.0: 2441 length of query: 26 length of database: 2,863,827,885 effective RSP length: 17 effective length of query: 9 effective length of database: 2,850,098,736 effective search space: 25650888624 effective search space used: 25650888624 T: 0 A: 30 X1: 6 (11.9 bits) X2: 15 (29.7 bits)

Table 12. The other animals belonging to distantly related species analyzed by our primers to demonstrate its universal nature

SN.	Name of the animal
1.	Indian black buck no.1
2.	Indian black buck no 2
3	sheep
4	pig
5	dog
6	chimpanzee (chimss)
7	human (humsk)
8	Hamster
9	crocodile no l
10	crocodile no2
11	turtle nol
12	turtle no2
13	mouse
14	varanus
15	Naga-naga snake
16	Indian elephant
17	hen
18	dugong
19	lizard
20	weaver bird not
21	weaver bird no2
22	buffalo no l
23	buffalo no 2

CLAIMS

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1 Universal primers named as 'mcb 398' and 'mcb 869' capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level, said primers, having the sequences:

primers name Sequence (5'-3')

mcb 398 "TACCATGAGGACAAATATCATTCTG"

mcb 869 "CCTCCTAGTTTGTTAGGGATTGATCG

- 2. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is capable of significantly discriminating amongst various evolutionary lineages of different animal species.
 - 3. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is flanked by the highly conserved sequences amongst a vast range of animal species.
- 4. Primers as claimed in claim 1 wherein the fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.
 - 5. Primers as claimed in claim 1 wherein in Antilope cervicapra species, the sequences of the fragment mentioned under claim 1 are as follows:
- - 6. A method for the identification of the animal from a biological sample, said method comprising the steps of:
 - a) isolating and amplifying the DNA from the biological sample to be tested using the primers as claimed in claim 1,
 - b) sequencing the amplified products,
 - c) blasting the sequence resolved in step (b) against mito database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely family of the animal source of the biological sample.

- d) blasting the sequence resolved in step (b) against non-redundant (nr) database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely genus, species or more precisely the sub-species of the animal source of the biological sample,
- e) identifying the most significant alignment of the sequence resolved with cytochrome b gene sequence of the animal identified in steps (c) and (d) respectively and selection of these animals as 'reference animals' for further studies,

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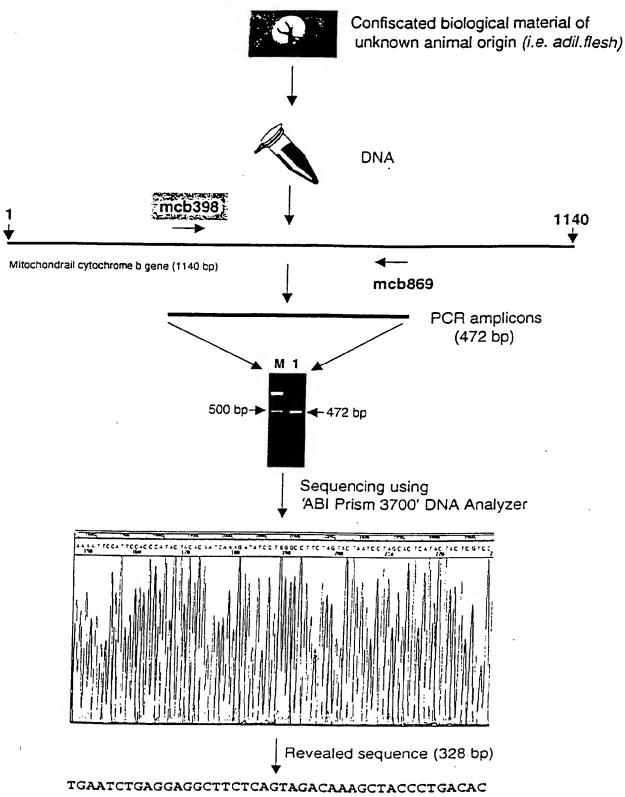
- f) isolating and amplifying and sequencing the DNA sequences from the reference animal on both strands in triplicate using the primers as claimed in claim 1,
- g) aligning the sequences obtained using CLUSTRAL program and identifying the variable sites amongst the animals analyzed,
- h) comparing the nucleotide sequences pair-wise to determine the variation among the animals resolved and identifying the nucleotide sequence to which the DNA sequence of the biological sample bears maximum similarity as the source animal of the biological sample.
- 7. A method as claimed in claim 6 wherein the universal PCR protocol works universally with the DNA template of any unknown animal origin and the universal primers mentioned under column 4.
- 8. A method as claimed in claim 6 wherein the Amplification reactions should be carried out in 20 μl reaction volume containing approximately 20 ηg of template DNA, 100μm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl₂, 0.5 unit of Ampli*Taq* Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35th cycles should be held for 10 min.
- 9. A method as claimed in claim 6 wherein the method enables identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.
- 10. A method as claimed in claim 6 wherein the method is used for animal identification to establish the crime with the criminal beyond a reasonably doubt.
- 11. A method as claimed in claim 6 wherein the method is used to establish the identity of

- biological materials such as skin, homs etc confiscated from animal poachers, if it is that of an endangered species.
- 12. A method as claimed in claim 6 wherein the method is used for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation of the wildlife resources could be controlled.

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- 13. A method as claimed in claim 6 wherein the method is used to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented.
- 10 14. A method as claimed in claim 6 wherein the method is used for animal identification to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies.
 - 15. A method as claimed in claim 6 wherein the method is used to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.
- 16. A method as claimed in claim 6 wherein the method is used so that it can be converted to a (a) <u>COMMERCIAL 'MOLECUALR KIT'</u> and (b) <u>'DNA CHIPS'</u> based applications for wildlife identification in forensics.



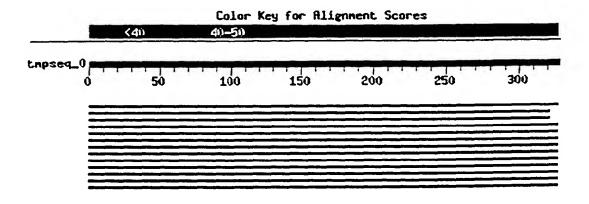
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AACAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCAT
TCCACCCATACTACACAATCAAAGATATCCTGGGCCTTCTAGT
ACTAATCCTAGCACTCATACTACTCGTCCTATTCTCACCAGAC
CTGTTAGGAGACCCCGATAACTACATCCCTGCCAACCCTCTAA
ATACCCCTCCCCATATCAAGCCTGAAT

Figure 1 a

Sequence of cytochrome b gene (328 bp) revealed from biological material of unknown origin i.e. 'adil.flesh' using primers 'mcb398' and 'mcb869'

Homology search in 'nr' database using 'BLAST'

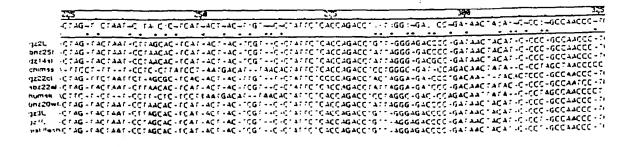
http://www.ncbi.nlm.nih.gov/BLAST/



	Score	E
Sequences producing significant alignments:	(bits)	Value
gb[AY005809.1] Panthera pardus cytochrome b gene, partial c	. 603	e-170
gb AF053054.1 AF053054 Panthera tigris sumatrae isolate Su1	527	e-147
gb AF053053.1 AF053053 Panthera tigris tigris isolate B7 mi	527	e-147
ablAF053050.1 AF053050 Panthera tigris corbetti isolate C2	476	e-132
gb AF053049.1 AF053049 Panthera tigris corbetti isolate C1	476	e-132

Selection of reference animals based on above information and further analysis using primers 'mcb398' and 'mcb869'

Multiple sequence alignments using 'Autoassembler'



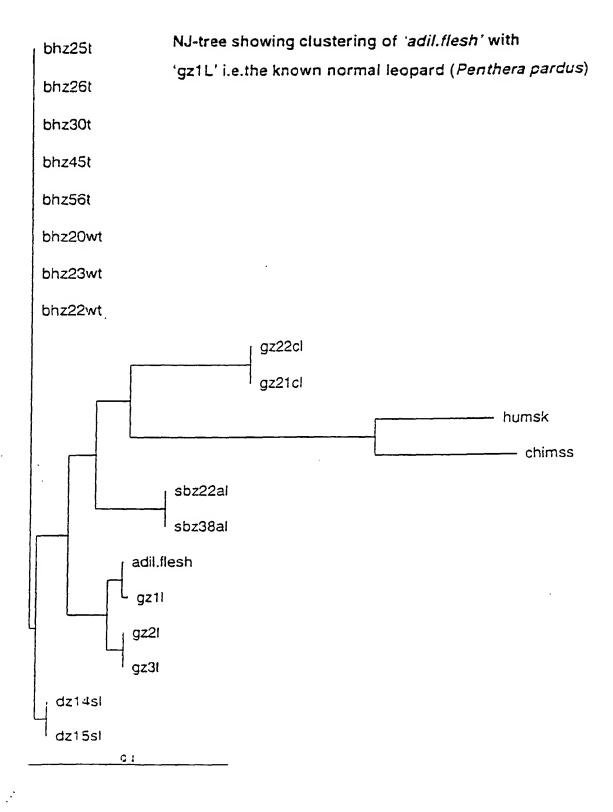


Figure 1c

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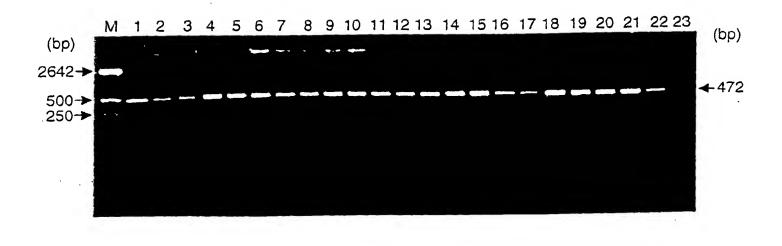


Figure 2

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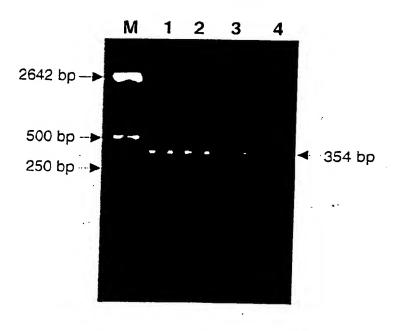


Figure 3

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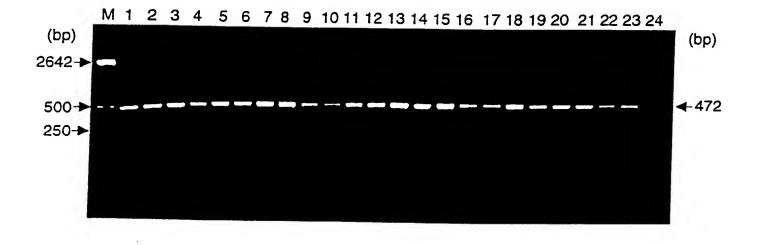


Figure 4

INTERNATIONAL SEARCH REPORT

inte Application No PC 1/11N 01/00055

A. CLASSIFICATION OF SUBJECT MATTER IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

 $\begin{array}{ccc} \text{Minimum documentation searched (classification system followed by classification symbols)} \\ \text{IPC 7} & \text{C12Q} \end{array}$

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EPO-Internal, EMBL, WPI Data, PAJ, MEDLINE, EMBASE

Category °	Cilation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KOCHER T D ET AL: "DYNAMICS OF MITOCHONDRIAL DNA EVOLUTION IN ANIMALS AMPLIFICATION AND SEQUENCING WITH CONSERVED PRIMERS" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES, vol. 86, no. 16, 1989, pages 6196-6200, XP002189444 1989 ISSN: 0027-8424 the whole document	1-16
Y	WO 92 05277 A (DAVIDSON WILLIAM SCOTT;BARTLETT SYLVIA ERNESTINE (CA)) 2 April 1992 (1992-04-02) the whole document/	1-16

Further documents are listed in the continuation of box C.	Patent family members are listed in annex.	
Special categories of cited documents: A* document defining the general state of the art which is not considered to be of particular relevance E* earlier document but published on or after the international filing date L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) O* document referring to an oral disclosure, use, exhibition or other means P* document published prior to the international filing date but later than the priority date claimed	 'T' later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention 'X' document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone 'Y' document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art. '&' document member of the same patent family 	
Date of the actual completion of the international search	Date of mailing of the international search report	
28 February 2002	12/03/2002	
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer Hagenmaier, S	

INTERNATIONAL SEARCH REPORT

Internal Application No

	<u> </u>				
(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT ategory © Citation of document, with indication, where appropriate, of the relevant passages Relevant to claim No.					
Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.				
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